

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hadlaczky, Gyula
Szalay, Aladar

(ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Heller Ehrman White & McAuliffe
(B) STREET: 4350 La Jolla Village Drive, 6th Floor
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92122

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/835,682
(B) FILING DATE: 10-APR-1997
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/695,191
(B) FILING DATE: 07-AUG-1996
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/682,080
(B) FILING DATE: 15-JUL-1996
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/629,822
(B) FILING DATE: 10-APR-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 24601-402I

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 858-450-8403
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTTNCCATGA	TTTTAAGTTT	60
TCTCGCCATA	TTCCTGGTCC	TACAGTGTGC	ATTTCTCCAT	TTTNCACGTT	TTNCAGTGAT	120
TTCGTCAATT	TCAAGTCCTC	AAGTGGATGT	TTCTCATTTN	CCATGAATTT	CAGTTTTCTN	180
GCCATATTTC	ACGTCTCTAA	GNGGACATTT	CTAAATTTNC	CACCTTTTTC	AGTTTTCTCT	240
GCCATATTTC	ACGTCTCTAA	ATGTGTATTT	CTCGTTTNCC	GTGATTTTCA	GTTTTCTCGC	300
CAGATTCCAG	GTCTCTATA	GTGCATTTCT	CATTTNNCAC	GTTTTTCAGT	GATTTTCGTC	360
TTTTTTTCA	TCGGCAAGTG	GATGTTTCTC	ATTTNCCATG	ATTTNCAGTT	TTCTTGNAAT	420
ATTCATGTGC	CTACAATGAT	CATTTTAAAT	TTTCCACCTT	TTTCAATTTT	CACGCCATAT	480
TTCATGTCTC	AAAGTGTCTA	TTTCTCCTTT	TCCGCGATTT	TCAGTTTCTT	CGCCATATTC	540
CAGGTCCTAC	AGTGTGCATT	CCTCATTTT	CACCTTTTTC	ACTGATTTTC	TCATTTTTC	600
AGTCGTCAAC	TGGATCTTTC	TAATTTTCCA	TGATTTTTCAG	TTATCTTGTC	ATATTCCATG	660
TCCTACAGTG	GACATTTCTA	AATTTTCCAA	CTTTTTCAT	TTTTCTCGAC	ATATTGACG	720
TGCTAAAGTG	TGTATTTCTT	ATTTTCCGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCAGGTC	780
CTAATAGTGT	GCATTTCTCA	TTTTTCACGT	TTTTTCAGTGA	TTTCGTCATT	TTTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	TGTCAGTTTT	CTTGCTATAT	TCCATGTCCT	900
ACAGTGACAT	TTCTAAATAT	TATACCTTTT	TCAGTTTTTTC	TCACCATAT	TCACGTCCTA	960
AAGTATATAT	TTCTCATTTT	CCCTGATTTT	CAGTTTCTCT	GCCATATTCC	AGGTCCTACA	1020
GTGTGCATTT	CTCATTTTTC	ACGTTTTTCA	GTAATTTCTT	CATTTTAAAT	GCCCTCAAAT	1080
GGATGTTTCT	CATTTTCCAT	GATTTTCAGT	TTTCTTGCCA	TATACCATGT	CCTACAGTGG	1140
ACATTTCTAA	ATTATCCACC	TTTTTCAGTT	TTTCATCGGC	ACATTTACAG	TCCTAAAGTG	1200
TGTATTTCTA	ATTTTCAGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGAC	CTACAGTGTG	1260
CATTTCTCAT	TTTTTCACGTT	TTTCAGTGAA	TTC			1293

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1044 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCATATG	TGAAAAAGGA	AATATCTTCC	CCTGAAAAC	AGACAGAAGG	ATTCTCAGAA	60
TCTTATTTGT	GATGTGCGCC	CCTCAACTAA	CAGTGTGAA	GCTTTCTTTT	GATAGAGCAG	120
TTTTGAAACA	CTCTTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTT	180
CGTTGGAAAC	GGGATTGTCT	TCATATAAAC	CCTAGACAGA	AGCATTCTCA	GAAGCTTCAT	240
TGGGATGTTT	CAGTTGAAGT	CACAGTGTTG	AACAGTCCCC	TTTCATAGAG	CAGGTTTGAA	300
ACACTCTTTT	TTGTAGTATC	TGGAAGTGGA	CATTGTGGAG	GATCTCAGGA	CTGCGGTGAA	360
AAAGGAAATA	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACCTT	CCTTTGAGAG	AGCAGTTTTC	AAACACTCTT	480
TTTGTGGAAT	CTGCAAGTGG	ATATTGTCTT	AGCTTTGAGG	ATTTTCGTTG	GAAACGGGAT	540
TACATATAAA	AAGCAGACAG	CAGCATTTCC	AGAACTTCTT	TTGTGATGTT	TGCATTCAAG	600
TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTTGAA	ACACACTTTT	TGATGTATCT	660
GGATGTGGAC	ATTTGCAGCG	CTTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TTCCCCTGAA	720

AACTAGACAG	AAGCATTCTC	AGAAACTTAT	TTGTGATGTG	CGCCCTCAAC	TAACAGTGT	780
GAAGCTTTCT	TTTGATAGAG	GCAGTTTTGA	AACACTCTTT	TGTGGAATCT	GCAAGTGGAT	840
ATTTGTCTAG	CTTTGAGGAT	TTCTTTGGAA	ACGGGATTAC	ATATAAAAAG	CAGACAGCAG	900
CATTCCCAGA	ATCTTGTTTG	TGATGTTTGC	ATTCAAGTCA	CAGAGTTGAA	CATTCCCTTT	960
CAGAGAGCAG	GTTTGAACAC	TCTTTTTATA	GTATCTGGAT	GTGGACATT	GGAGCGCTTT	1020
CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2492 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	GCCCCTTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAAGG	GGGTGCAGGC	TGCATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
GGATCTATGG	GGGTGGGGAG	AAGCCCAGTG	ACAGTGCCTA	GAAGAGACAA	GGTGGCCTGA	180
GAGGGTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGGCCAG	GTCTCAAGCA	GGAAGTGAGG	240
AATGGGACAG	GCTTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGGT	300
TGCTATCCTG	GGTTTCAACC	CCCCAGGTTG	AAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTGT	TCAAATCCAA	480
AGGGCCCCCTG	CTGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCTGGGC	CACACGCGTT	540
TAGGGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
TTTCCACCTA	TTCGAAACAA	TCACATAAAA	TCCATCCTGG	AAAAAGCCTG	GGGGATGGCA	660
CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGGTT	TAGGGTTAGG	720
GATCAACGTT	GGTTAGGAGT	TAGGGATACA	GTAGGGTACC	GGTAGGGTTA	GGGGTTAGGG	780
TTAGGGGTTA	GGGTTAGGGT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTTAGGGTTA	840
GGGTTAGGTT	TTGGGGTGCG	GTATTTTGGT	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
AGAGTTCTTG	TTTTTCCTTC	AGCAATTTGT	CATTTTTTAA	AGAGTTTAGC	AATTCTAACA	960
GATATAGACC	AGCTGTGCTA	TCTCATTGTG	GTTTTCAATT	GTAACCACAT	TGTGGTTTCA	1020
ATGTGTTTAC	TTGCCATCTG	TAGATCTTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGTG	1080
CATTTCCTGN	NTTTNGGCTG	TTTAACTTAT	TGTTTAGTTT	TAATAATTTT	TTATATATTT	1140
GAAGACAAAT	CTTTCTCAGA	TGTGTATTTG	CAAAATTTTC	TTCAATATGA	GGCTTGCTTT	1200
TGTCTCTAAC	AAGGTCTCTT	CAGAGATAAC	TTAAATATAA	GAAATCCACA	CTGTCAC TTC	1260
TTTTGTGTAT	ATCTACCTTT	TGTGTCATTT	GTTAAATTC	ATTACCAAAC	CCAAAGGCAG	1320
ATAGCTTTTC	TTCTATTGTT	TCTTCTAGAA	ATTTGTATAG	TTTTGCATTT	TTAGTGTAAG	1380
GATGATTTTG	AGTGATTATT	TGTGTAAGTT	GTAAAGTTTT	CGTCTATATC	CATATCATTT	1440
CTTATGGTTT	CCAATTAATC	GTTCCCTCAC	TATTTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCCTCCTGG	AAAAGGGAAA	1560
GTCTGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTCACA	TATTAGTAGC	ATCTCTAGTG	1620
CTGGAGTGGA	TGGGCACTTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCATTC	ACTCTGCAAT	AAAAATGTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAAGA	GGCAGGCGCA	GTAGGTACAA	1860
ACGTGATCGC	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCCA	GAGTGGATT	1920
GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCCACAA	GCCTAAGTGG	1980
GGCAAGTTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACCAGAC	AAAGAAAACA	GGTGGAGACT	2040
TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAAT	TCCCTGCACA	GGACTCTTAG	2100
GCTGTTTAAT	GCATCGCTCA	GTCCCACTCC	TCCCTATTTT	TCTACAATAA	ACTCTTTTACA	2160
CTGTGTTTCT	TTTCAATGAA	GTTATCTGCC	ATCTTTGTAT	TGCCTCTTGG	TGAAAATGTT	2220
TCTTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCCC	AGTAATAGCT	CCGTTTCAGT	2280
TTGAATTTAC	AGAAGCTGATG	GGCTTAATAA	CTGGCGCTCT	GACTTTAGTG	GTGCAGGAGG	2340

CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCCGAG GTGGCGGCTG 2400
 CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG 2460
 ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG 2492

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA TTGGGATGTT TCAGTTGA 28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA 29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC

(2) INFORMATION FOR SEQ ID NO:7:

- ```
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
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(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTTAAAT TAATTAAGCC CGGGC

25

(2) INFORMATION FOR SEO ID NO: 8:

(i) SEOUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: .

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(D) OTHER INFORMATION IL-2 signal sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT  
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT  
Val Thr Asn Ser Ala Pro Thr

69

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 945 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...942

(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGC | TTA | AAG | ATG | ACT | TCG | AAA | GTT | TAT | GAT | CCA | GAA | CAA | AGG | AAA | CGG | 48  |
| Ser | Leu | Lys | Met | Thr | Ser | Lys | Val | Tyr | Asp | Pro | Glu | Gln | Arg | Lys | Arg |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| ATG | ATA | ACT | GGT | CCG | CAG | TGG | TGG | GCC | AGA | TGT | AAA | CAA | ATG | AAT | GTT | 96  |
| Met | Ile | Thr | Gly | Pro | Gln | Trp | Trp | Ala | Arg | Cys | Lys | Gln | Met | Asn | Val |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| CTT | GAT | TCA | TTT | ATT | AAT | TAT | TAT | GAT | TCA | GAA | AAA | CAT | GCA | GAA | AAT | 144 |
| Leu | Asp | Ser | Phe | Ile | Asn | Tyr | Tyr | Asp | Ser | Glu | Lys | His | Ala | Glu | Asn |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| GCT | GTT | ATT | TTT | TTA | CAT | GGT | AAC | GCG | GCC | TCT | TCT | TAT | TTA | TGG | CGA | 192 |
| Ala | Val | Ile | Phe | Leu | His | Gly | Asn | Ala | Ala | Ser | Ser | Tyr | Leu | Trp | Arg |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CAT | GTT | GTG | CCA | CAT | ATT | GAG | CCA | GTA | GCG | CGG | TGT | ATT | ATA | CCA | GAT | 240 |
| His | Val | Val | Pro | His | Ile | Glu | Pro | Val | Ala | Arg | Cys | Ile | Ile | Pro | Asp |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| CTT | ATT | GGT | ATG | GGC | AAA | TCA | GGC | AAA | TCT | GGT | AAT | GGT | TCT | TAT | AGG | 288 |
| Leu | Ile | Gly | Met | Gly | Lys | Ser | Gly | Lys | Ser | Gly | Asn | Gly | Ser | Tyr | Arg |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| TTA | CTT | GAT | CAT | TAC | AAA | TAT | CTT | ACT | GCA | TGG | TTG | AAC | TTC | TTA | ATT | 336 |
| Leu | Leu | Asp | His | Tyr | Lys | Tyr | Leu | Thr | Ala | Trp | Leu | Asn | Phe | Leu | Ile |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| TAC | CAA | AGA | AGA | TCA | TTT | TTT | GTC | GGC | CAT | GAT | TGG | GGT | GCT | TGT | TTG | 384 |
| Tyr | Gln | Arg | Arg | Ser | Phe | Phe | Val | Gly | His | Asp | Trp | Gly | Ala | Cys | Leu |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| GCA | TTT | CAT | TAT | AGC | TAT | GAG | CAT | CAA | GAT | AAG | ATC | AAA | GCA | ATA | GTT | 432 |
| Ala | Phe | His | Tyr | Ser | Tyr | Glu | His | Gln | Asp | Lys | Ile | Lys | Ala | Ile | Val |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| CAC | GCT | GAA | AGT | GTA | GTA | GAT | GTG | ATT | GAA | TCA | TGG | GAT | GAA | TGG | CCT | 480 |
| His | Ala | Glu | Ser | Val | Val | Asp | Val | Ile | Glu | Ser | Trp | Asp | Glu | Trp | Pro |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| GAT | ATT | GAA | GAA | GAT | ATT | GCG | TTG | ATC | AAA | TCT | GAA | GAA | GGA | GAA | AAA | 528 |
| Asp | Ile | Glu | Glu | Asp | Ile | Ala | Leu | Ile | Lys | Ser | Glu | Glu | Gly | Glu | Lys |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| ATG | GTT | TTG | GAG | AAT | AAC | TTC | TTC | GTG | GAA | ACC | ATG | TTG | CCA | TCA | AAA | 576 |
| Met | Val | Leu | Glu | Asn | Asn | Phe | Phe | Val | Glu | Thr | Met | Leu | Pro | Ser | Lys |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| ATC | ATG | AGA | AAG | TTA | GAA | CCA | GAA | GAA | TTT | GCA | GCA | TAT | CTT | GAA | CCA | 624 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Met | Arg | Lys | Leu | Glu | Pro | Glu | Glu | Phe | Ala | Ala | Tyr | Leu | Glu | Pro |     |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |
| TTC | AAA | GAG | AAA | GGT | GAA | GTT | CGT | CGT | CCA | ACA | TTA | TCA | TGG | CCT | CGT | 672 |  |
| Phe | Lys | Glu | Lys | Gly | Glu | Val | Arg | Arg | Pro | Thr | Leu | Ser | Trp | Pro | Arg |     |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |  |
| GAA | ATC | CCG | TTA | GTA | AAA | GGT | GGT | AAA | CCT | GAC | GTT | GTA | CAA | ATT | GTT | 720 |  |
| Glu | Ile | Pro | Leu | Val | Lys | Gly | Gly | Lys | Pro | Asp | Val | Val | Gln | Ile | Val |     |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |  |
| AGG | AAT | TAT | AAT | GCT | TAT | CTA | CGT | GCA | AGT | GAT | GAT | TTA | CCA | AAA | ATG | 768 |  |
| Arg | Asn | Tyr | Asn | Ala | Tyr | Leu | Arg | Ala | Ser | Asp | Asp | Leu | Pro | Lys | Met |     |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |
| TTT | ATT | GAA | TCG | GAT | CCA | GGA | TTC | TTT | TCC | AAT | GCT | ATT | GTT | GAA | GGC | 816 |  |
| Phe | Ile | Glu | Ser | Asp | Pro | Gly | Phe | Phe | Ser | Asn | Ala | Ile | Val | Glu | Gly |     |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |  |
| GCC | AAG | AAG | TTT | CCT | AAT | ACT | GAA | TTT | GTC | AAA | GTA | AAA | GGT | CTT | CAT | 864 |  |
| Ala | Lys | Lys | Phe | Pro | Asn | Thr | Glu | Phe | Val | Lys | Val | Lys | Gly | Leu | His |     |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |  |
| TTT | TCG | CAA | GAA | GAT | GCA | CCT | GAT | GAA | ATG | GGA | AAA | TAT | ATC | AAA | TCG | 912 |  |
| Phe | Ser | Gln | Glu | Asp | Ala | Pro | Asp | Glu | Met | Gly | Lys | Tyr | Ile | Lys | Ser |     |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |  |
| TTC | GTT | GAG | CGA | GTT | CTC | AAA | AAT | GAA | CAA | TAA |     |     |     |     |     | 945 |  |
| Phe | Val | Glu | Arg | Val | Leu | Lys | Asn | Glu | Gln |     |     |     |     |     |     |     |  |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |     |  |

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG

30

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTAC

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| CCTCCACGCA | CGTTGTGATA | TGTAGATGAT | AATCATTATC | AGAGCAGCGT | TGGGGGATAA | 60   |
| TGTCGACATT | TCCACTCCCA | ATGACGGTGA | TGTATAATGC | TCAAGTATTC | TCCTGCTTTT | 120  |
| TTACCACTAA | CTAGGAAGTG | GGTTTGGCCT | TAATTCAGAC | AGCCTTGGCT | CTGTCTGGAC | 180  |
| AGGTCCAGAC | GACTGACACC | ATTAACACTT | TGTCAGCCTC | AGTGACTACA | GTCATAGATG | 240  |
| AACAGGCCTC | AGCTAATGTC | AAGATACAGA | GAGGTCTCAT | GCTGGTTAAT | CAACTCATAG | 300  |
| ATCTTGTTCA | GATACAATA  | GATGTATTAT | GACAAATAAC | TCAGCAGGGA | TGTGAACAAA | 360  |
| AGTTTCCGGG | ATTGTGTGTT | ATTTCATTTC | AGTATGTTAA | ATTTACTAGG | ACAGCTAATT | 420  |
| TGTCAAAAAG | TCTTTTTCAG | TATATGTTAC | AGAATTGGAT | GGCTGAATTT | GAACAGATCC | 480  |
| TTCGGGAATT | GAGACTTCAG | GTCAACTCCA | CGCGCTTGGA | CCTGTCGCTG | ACCAAAGGAT | 540  |
| TACCCAATTG | GATCTCCTCA | GCATTTTCTT | TCTTTAAAAA | ATGGGTGGGA | TTAATATTAT | 600  |
| TTGGAGATAC | ACTTTGCTGT | GGATTAGTGT | TGCTTCTTTG | ATTGGTCTGT | AAGCTTAAGG | 660  |
| CCCAAACTAG | GAGAGACAAG | GTGTTATTGT | CCCAGGCGCT | TGCAGGACTA | GAACATGGAG | 720  |
| CTTCCCCTGA | TATATGGTTA | TCTATGCTTA | GGCAATAGGT | CGCTGGCCAC | TCAGCTCTTA | 780  |
| TATCCACGCA | GGCTAGTCTC | ATTGTACGGG | ATAGAGTGAG | TGTGCTTCAG | CAGCCCAGAG | 840  |
| GAGTTGCAAG | GCTAAGCACT | GCAATGGAAA | GGCTCTGCGG | CATATATGTG | CCTATTCTAG | 900  |
| GGGGACATGT | CATCTTTCAT | GAAGGTTTCA | TGTCCTAGTT | CCCTTCCCCC | AGGCAAAACG | 960  |
| ACACGGGAGC | AGGTCAGGGT | TGCTCTGGGT | AAAAGCCTGT | GAGCCTGGGA | GCTAATCCTG | 1020 |
| TACATGGCTC | CTTTACCTAC | ACACTGGGGA | TTTGACCTCT | ATCTCCACTC | TCATTAATAT | 1080 |
| GGGTGGCCTA | TTTGCTCTTA | TTAAAAGGAA | AGGGGGAGAT | GTTGGGAGCC | GCGCCCACAT | 1140 |
| TCGCCGTTAC | AAGATGGCGC | TGACAGCTGT | GTTCTAAGTG | GTAAACAAAT | AATCTGCGCA | 1200 |
| TGTGCCGAGG | GTGGTTCTTC | ACTCCATGTG | CTCTGCCTTC | CCCGTGACGT | CAACTCGGCC | 1260 |
| GATGGGCTGC | AGCCAATCAG | GGAGTGACAC | GTCTAGGCG  | AAGGAGAATT | CTCCTTAATA | 1320 |
| GGGACGGGGT | TTCGTTCTCT | CTCTCTCTCT | TGCTTCTCTC | TCTTGCTTTT | TCGCTCTCTT | 1380 |
| GCTTCCCGTA | AAGTGATAAT | GATTATCATC | TACATATCAC | AACGTGCGTG | GAGG       | 1434 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| CCTCCACGCA | CGTTGTGATA  | TGTAGATGAT | AATCATTATC | AGAGCAGCGT | TGGGGGATAA | 60  |
| TGTCGACATT | TCCACTCCCA  | ATGACGGTGA | TGTATAATGC | TCAAGTATTC | TCCTGCTTTT | 120 |
| TTACCACTAA | CTAGGAAGTG  | GGTTTGGCCT | TAATTCAGAC | AGCCTTGGCT | CTGTCTGGAC | 180 |
| AGGTCCAGAT | ACAACATAGAT | GTATTATGAC | AAATAACTCA | GCAGGGATGT | GAACAAAAGT | 240 |



|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| TTCCGGGATT | GCGTGTATT   | TCCATCCAGT | ATGTTAAATT | TACTAGGGCA | GCTAATTTGT | 300  |
| CAAAAAGTCT | TTTCCAGTAT  | ATGTTACAGA | ATTGGATGGC | TGAATTTGAA | CAGATCCTTC | 360  |
| GGGAATTGAG | ACTTCAGGTC  | AACTCCACGC | GCTTGGACCT | GTCCCTGACC | AAAGGATTAC | 420  |
| CCAATTGGAT | CTCCTCAGCA  | TTTTCTTTCT | TTAAAAAATG | GGTGGGATTA | ATATTATTTG | 480  |
| GAGATACT   | TTGCTGTGGA  | TTAGTGTTC  | TTCTTTGATT | GGTCTGTAAG | CTTAAGGCCC | 540  |
| AAACTAGGAG | AGACAAGGTG  | GTTATTGCCC | AGGCGCTTGC | AGGACTAGAA | CATGGAGCTT | 600  |
| CCCCTGATAT | ATCTATGCTT  | AGGCAATAGG | TCGCTGGCCA | CTCAGCTCTT | ATATCCCATG | 660  |
| AGGCTAGTCT | CATTGCACGG  | GATAGAGTGA | GTGTGCTTCA | GCAGCCCGAG | AGAGTTGCAC | 720  |
| GGCTAAGCAC | TGCAATGGAA  | AGGCTCTGCG | GCATATATGA | GCCTATTCTA | GGGAGACATG | 780  |
| TCATCTTTCA | AGAAGGTTGA  | GTGTCCAAGT | GTCTTCTCTC | CAGGCAAAAC | GACACGGGAG | 840  |
| CAGGTCAGGG | TTGCTCTGGG  | TAAAAGCCTG | TGAGCCTAAG | AGCTAATCCT | GTACATGGCT | 900  |
| CCTTTACCTA | CACACTGGGG  | ATTGACCTC  | TATCTCCACT | CTCATTAATA | TGGGTGGCCT | 960  |
| ATTTGCTCTT | ATTAAAAGGA  | AAGGGGGAGA | TGTTGGGAGC | CGCGCCACA  | TTCGCCGTTA | 1020 |
| CAAGATGGCG | CTGACAGCTG  | TGTTCTAAGT | GGTAAACAAA | TAATCTGCGC | ATGCGCCGAG | 1080 |
| GGTGGTTCTT | CACTCCATGT  | GCTCTGCCTT | CCCCGTGACG | TCAACTCGGC | CGATGGGCTG | 1140 |
| CAGTCAATCA | GGGAGTGACA  | CGTCCTAGGC | GAAGGAAAAT | TCTCCTTAAT | AGGGACGGGG | 1200 |
| TTTCGTTTTT | TCTCTCTCTT  | GCTTCGCTCT | CTCTTGCTTC | TTGCTCTCTT | TTCCTGAAGA | 1260 |
| TGTAAGAATA | AAGCATTTGCC | GCAGAAGATT | CTGGTCTGTG | GTGTTCTTCC | TGGCCGGTCG | 1320 |
| TGAGAACGCG | TCTAATAACA  | ATTGGTGCCG | AAACCCGGGT | GATAATGATT | ATCATCTACA | 1380 |
| TATACAACG  | TGCGTGGAGG  |            |            |            |            | 1400 |

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1369 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| CCTCCACGCA  | CGTTGTGATA | TGTAGATGAT | AATCATTATC  | ACTTTACGGG | TCCTTTCACT | 60   |
| ACAACCTGCCA | CGAGGCCCCG | TGCTCTGGTA | ATAGATCTTT  | GCTGAAAAGG | CACACACATG | 120  |
| ACACATTACT  | CAAGGTGGGC | TCATCTGAGC | TGCAGATTCA  | GCTTAATATG | AATCTTGCCA | 180  |
| ATTGTGTGAA  | ATCATAAATC | TTCAAAGTGA | CACCTATTGC  | CAGACACAGG | TGCCACCTT  | 240  |
| TGGCATAATA  | AACAAACACA | AATTATCTAT | TATATAAAGG  | GTGTTAGAAG | ATGCTTTAGA | 300  |
| ATACAAATAA  | ATCATGGTAG | ATAACAGTAA | GTTGAGAGCT  | TAAATTTAAT | AAAGTGATAT | 360  |
| ACCTAATAAA  | AATTAAATTA | AGAAGGTGTG | AATATACTAC  | AGTAGGTAAA | TTATTTCACT | 420  |
| AATTTATTTT  | CTTTCTTAAT | CCTTTATAAT | GTTTTCTGCT  | ATTGTCAATT | GCACATCCAT | 480  |
| ATGTTCAATT  | CTTCACTGTA | ATGAAGAAAT | GTAGTAAATA  | TACTTTCCGA | ACAAGTTGTA | 540  |
| TCAAATATGT  | TACACTTGAT | TCCGTGTGTT | ACTTATCATT  | TTATTATTAT | ATTGATTGCA | 600  |
| TTCTTTCGTT  | ACTTGATATT | ATTACAAGGT | ACATATTTAT  | TCTCTCAGAT | CTTCATTATA | 660  |
| CTCTAACCAT  | TTTATAACAT | ACTTTATTTA | TTCATTTCTT  | ATGTGTGCTG | TGAGGCACAA | 720  |
| ATGCCAGAGA  | GAACCTGAGC | AGATAAGAGG | ACAAATTGCA  | AGAGTCAGTT | ACCTCCTGCT | 780  |
| GTTCTTGGA   | AACTCAGGAT | CAAATTCAGG | TTGTCAGGCT  | TGGCAGCATG | CACTTTTTAC | 840  |
| CAGTGCCTCC  | ATCTTGCTAG | CCCTGAACAT | CAAGCTTTGC  | AGACAGACAG | GCTACACTAA | 900  |
| GTGAACCTGGT | CATTACAGC  | ATGCATGGTG | ATTTATTGTT  | ACTTTCTATT | CCATGCCTTT | 960  |
| ACTATTTCTA  | CTAGGTGCTA | GCTAGTACTG | TATTTTCGAGA | TAGAAGTTAC | TGAAAGAAAA | 1020 |
| TTACATTGTT  | TTCTATAGAT | CCTTGATACT | CTTTCAGCAG  | ATATAGAGTT | TTAATCAGGT | 1080 |
| CCTAGACCTT  | TTCTTCACTC | TTATTAAATA | CTAAGTACAA  | ATTAAGTTTA | TCCAAAACAG | 1140 |
| TACGGATGTT  | GATTTTGTGC | AGTTCTACTA | TGATAATAGT  | CTAGCTTCAT | AAATCTGACA | 1200 |
| CACTTATTGG  | GAATGTTTTT | GTTAATAAAA | GATTCAGGTG  | TTACTCTAGG | TCAAGAGAAT | 1260 |
| ATTAAACATC  | AGTCCCAAAT | TACAAACTTC | AATAAAAGAT  | TTGACTCTCC | AGTGGTGGCA | 1320 |
| ATATAAAGTG  | ATAATGATTA | TCATCTACAT | ATCACAACGT  | GCGTGGAGG  |            | 1369 |

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22118 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|        |        |         |         |         |         |        |        |        |        |        |          |      |
|--------|--------|---------|---------|---------|---------|--------|--------|--------|--------|--------|----------|------|
| GAATTC | CCCT   | ATCCCT  | TAATC   | CAGATT  | GGTG    | GAATAA | CTTG   | GTATAG | ATGT   | TTGTGC | ATTA     | 60   |
| AAAACC | CTGT   | AGGATC  | TTTCA   | CTCTAG  | GTCA    | CTGTTC | CAGCA  | CTGGA  | ACCTG  | AATTGT | GGGCC    | 120  |
| CTGAGT | GATA   | GGTCCT  | TGGGA   | CATATG  | CAGT    | TCTGC  | CACAGA | CAGAC  | CAGACA | GACAG  | CAGACA   | 180  |
| CAGAC  | CAGACA | GACAG   | ACGTT   | ACAAAC  | AAAC    | ACGTTG | AGCC   | GTGTG  | CCAAC  | ACAC   | CACACAA  | 240  |
| ACACCA | CTCT   | GGCCATA | AATT    | ATTGAG  | GACG    | TTGATT | TATT   | ATTCTG | TGTT   | TGTG   | AGTCTG   | 300  |
| TCTGT  | CTGTC  | TGTCTG  | TCTG    | TCTGT   | CTGTC   | TATCAA | ACCA   | AAAGAA | ACCA   | AACA   | ATTATG   | 360  |
| CCTGC  | CTGCC  | TGCCTG  | CCCTG   | CCTACA  | CAGA    | GAAATG | ATTT   | CTTCAA | TCAA   | TCTAAA | ACGA     | 420  |
| CCTCCT | AAGT   | TTGCCT  | TTTTT   | TCTCTT  | TCTT    | TATCTT | TTTTT  | TTTTTT | TCTT   | TCTT   | CTCCT    | 480  |
| TCCTTC | CTTCT  | CTTCTT  | CTTCT   | TCCTTC  | CTTCT   | CTTTCT | TTTTT  | TTCTTT | CTTT   | CTTACT | TTTCT    | 540  |
| TTCTTT | CTTCT  | TTACTAT | TTA     | TTCTTT  | TCAT    | ACATAG | TTTTT  | TTAGTG | TAAAG  | CATCC  | CTGAC    | 600  |
| TGTCTT | TGAAG  | ACACTT  | TGTA    | GGCTCA  | ATC     | CTGTA  | AAGAGC | CTTCCT | CTGC   | TTTTCA | AATG     | 660  |
| CTGGC  | CATGAA | TGTTGT  | TACCT   | CACTAT  | GACC    | AGCTTA | GTCT   | TCAAGT | CTGA   | GTTACT | TGGAA    | 720  |
| AGGAG  | TTCCA  | AGAAG   | ACTGG   | TTATA   | TTTTT   | CATTTA | TATTAT | TGCATT | TTTAA  | TTAAAA | TTTA     | 780  |
| ATTTCA | CCAA   | AAGAAT  | TTAG    | ACTGA   | CCAAT   | TCAGAG | TCTG   | CCGTTT | AAAAA  | GCATA  | AAGGAA   | 840  |
| AAAGT  | AGGAG  | AAAAA   | CGTGA   | GGCTGT  | CTGT    | GGATGG | TCTGA  | GGCTG  | CTTTA  | GGGAG  | CCTCG    | 900  |
| TCACCA | TTCT   | GCACTT  | TCAA    | ACCGG   | GCCAC   | TAGA   | ACCCGG | TGAAG  | GGGAGA | AACCA  | AAGCG    | 960  |
| ACCTG  | GAAAC  | AATAGG  | TAC     | ATGA    | AGGCCA  | GCCAC  | CTCCA  | TCTTGT | TGTG   | CGGG   | AGTTCA   | 1020 |
| GTTAG  | CAGAC  | AAGATG  | GCTG    | CCATG   | CACAT   | GTTGT  | CTTTT  | AGCTT  | GGTGA  | GGTCA  | AAGTA    | 1080 |
| CAACC  | GAGTC  | ACAGA   | CAAG    | GAAGT   | TATACA  | CAGTG  | AGTTC  | CAGGT  | CAGCC  | AGAGT  | TTTACA   | 1140 |
| CAGAGA | AACC   | ACATCT  | TGAA    | AAAAA   | CAAAA   | AAATA  | AAATTA | AATAA  | ATATA  | ATTTA  | AAAAAT   | 1200 |
| TTAAAA | ATAG   | CCGGG   | AGTGA   | TGGCG   | CATGT   | CTTTA  | ATCCC  | AGCTC  | TCTC   | AGGC   | CAGAGAT  | 1260 |
| GGGAG  | GATTT  | CTGAG   | TTTGA   | GGCC    | AGCCTG  | GTCTG  | CAAAG  | TGAGT  | TCCAG  | GACAG  | TCAAG    | 1320 |
| GCTATA | CAGA   | GAAACC  | CTGT    | CTTGAAA | CT      | AAACT  | AAAT   | AAACT  | AAACT  | AAACT  | AAAAA    | 1380 |
| AATATA | AAAT   | AAAAA   | TTTTA   | AAGAA   | TTTTA   | AAAAA  | CTACA  | GAAAT  | CAAAC  | ATAAG  | CCCCAC   | 1440 |
| GAGAT  | TGGCAA | GTAAC   | TGCAA   | TCATAG  | CAGA    | AATATT | TATAC  | ACAC   | CACAC  | ACAC   | CAGACTC  | 1500 |
| TGTCAT | AAAAA  | TCCAAT  | TGTC    | CTTCAT  | GATG    | ATCAA  | ATTTT  | GATAG  | TCAGT  | AATA   | CTAGAA   | 1560 |
| GAATCA | TATG   | TCTG    | AAAAA   | AAAGC   | CAGAA   | CCTTTT | CTGC   | TTTTG  | TTTTT  | TTTG   | CCCCCA   | 1620 |
| AGATAG | GGTT   | TCTCT   | CAGTG   | TATCC   | CTGGC   | ATCCCT | GCCT   | GGAAC  | TTCTT  | TTGT   | AGGTTT   | 1680 |
| GGTAG  | CCTCA  | AACTC   | CAGAGA  | GGTCC   | TCTCT   | GCCTG  | CCTGC  | CTGCC  | TGCC   | GCCT   | GCCTGC   | 1740 |
| CTGCC  | TGCC   | GCCTG   | CTCA    | CTTCT   | TCTGC   | CACCC  | CACACA | ACCG   | AGTCGA | ACCT   | AGGATC   | 1800 |
| TTTATT | TTCTT  | TCTT    | TTCTC   | TCTT    | CTTCT   | TTCTT  | CTTTT  | CTTT   | CTTTT  | TTCTT  | CTTTT    | 1860 |
| CTTT   | CTTTT  | TTCTT   | ATTCA   | ATTAG   | TTTTT   | AATGTA | AAGTG  | TGTGT  | TTTGTG | CTCT   | ATCTGC   | 1920 |
| TGCC   | TATAG  | CTGCT   | TGCC    | AGGAG   | AGGGC   | AACGA  | AACCT  | AGGAG  | AAACC  | ACCAT  | GACGC    | 1980 |
| TCCTG  | AGAA   | AAGTG   | AAAAA   | ACAAC   | CAAAA   | AAGGA  | AAATC  | TAATC  | ACATA  | GAGT   | GATAGAT  | 2040 |
| ATATG  | CCGAG  | GCTGT   | CAGAG   | TGCTT   | TTTAA   | GGCTT  | AGTGT  | AAGTA  | ATGAA  | AATTG  | TGTGTG   | 2100 |
| TGTCT  | TTTTAT | CCAA    | ACACAG  | AAGAG   | AGGTG   | GCTCG  | GCCTG  | CATGT  | CTGTT  | GCTG   | CATGT    | 2160 |
| AGACC  | AGGCT  | GGCCT   | TGAAC   | ACATTA  | ATCT    | GTCTG  | CTCT   | GCTTC  | CCCTAA | TGCT   | GCGATT   | 2220 |
| AAAGG  | CATGT  | GCCAC   | CACTG   | CCCG    | ACTGA   | TTTCT  | TCTTT  | TTTTT  | TTTTT  | TGGA   | AAATAC   | 2280 |
| CTTT   | CTTTT  | TTTT    | TCTCT   | CTCTT   | TCTT    | CTTCT  | TTCTT  | TTCTT  | TTCTAT | TCTT   | TTTTT    | 2340 |
| TTTCT  | TTTTT  | TTTTT   | TTTTT   | TTTTT   | TTTAA   | AATTT  | TGCCTA | AGGTT  | TAAAGG | TGTG   | CTCCAC   | 2400 |
| AATTG  | CCTCA  | GCTCT   | GCTCT   | AATT    | TCTTT   | AAAAA  | AAAAA  | AAACA  | AAAAA  | AAA    | ACCAAAA  | 2460 |
| CAGTA  | TGTAT  | GTATG   | TATAT   | TTAGA   | AAGAA   | TACTA  | ATCCA  | TTAATA | AACTC  | TTTTT  | TCCTA    | 2520 |
| AAATT  | CATGT  | CATT    | CTTGTT  | CCACA   | AAAGTG  | AGTT   | CCAGGA | CTTACC | CAGAG  | AAACC  | CTGTG    | 2580 |
| TTCAA  | ATTTT  | TGTGT   | TCAAG   | GTCAC   | CTTG    | CTTACA | AAAGT  | GAGTT  | TCCAAG | TCCG   | ATAGGG   | 2640 |
| CTACA  | CAGAA  | AAACC   | ATATC   | TCAGA   | AAAAA   | AAAAA  | AGTTCC | AAAC   | CACAC  | ACAC   | CACAC    | 2700 |
| ACACA  | CACAC  | ACACA   | CACAC   | ACACA   | CACAC   | ACACA  | CACAG  | CGC    | CGCCG  | CGG    | GATGAGGG | 2760 |
| AAGTC  | GTGCC  | TAAA    | ATAAAT  | ATTTT   | TTCTGG  | CCAA   | AGTGAA | AGCAA  | ATCAC  | TATGA  | AGAGG    | 2820 |
| TACTC  | CTAGA  | AAAA    | ATAAAT  | ACAAA   | CGGGC   | TTTTT  | TAATCA | TTCC   | AGCACT | GTTT   | TGAATTT  | 2880 |
| AACT   | CTGAAT | TTAGT   | CTTGG   | AAA     | AGGGGGC | GGGT   | TGTGGT | GAGT   | GAGGGC | GAGC   | GAGCAG   | 2940 |
| ACGGG  | CGGGC  | GGG     | CGGGTGA | GTGGC   | CGGCG   | GCGG   | TGGCAG | CGAG   | CACCAG | AAA    | ACAACAA  | 3000 |
| ACCC   | CAAGCG | GTAG    | AGTGTT  | TTAAA   | AAATGA  | GACCT  | AAATG  | TGGT   | GGAACG | GAGG   | TCCGCCG  | 3060 |
| CCACC  | TCTCT  | CTT     | CACCTGC | TTAG    | TGCTC   | CCTT   | CCCCTT | ACTG   | TGCTCC | CTT    | CCCTAA   | 3120 |
| CTGTG  | CCCTAA | CTGTG   | CCCTGT  | TCCCT   | CAACC   | CGCTG  | ATTG   | CCAG   | CACGT  | ACTT   | TGACTT   | 3180 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| CAAGAACGAT  | TTTGCTGT    | TTCACCGCTC  | CCTGTCATAC  | TTTCGTTTTT  | GGGTGCCCGA  | 3240 |
| GTCTAGCCCG  | TTTCGCTATGT | TCGGGCGGGA  | CGATGGGGAC  | CGTTTGTGCC  | ACTCGGGAGA  | 3300 |
| AGTGGTGGGT  | GGGTACGCTG  | CTCCGTCGTG  | CGTGCGTGAG  | TGCCGGAACC  | TGAGCTCGGG  | 3360 |
| AGACCTCCG   | GAGAGACAGA  | ATGAGTGAGT  | GAATGTGGCG  | GCGCGTGACG  | GATCTGTATT  | 3420 |
| GGTTTGTATG  | GTTGATCGAG  | ACCATTGTCTG | GGCGACACCT  | AGTGGTGACA  | AGTTTCGGGA  | 3480 |
| ACGCTCCAGG  | CCTCTCAGGT  | TGGTGACACA  | GGAGAGGGAA  | GTGCCTGTGG  | TGAGGCGACC  | 3540 |
| AGGGTGACAG  | GAGGCCGGGC  | AAGCAGGCGG  | GAGCGTCTCG  | GAGATGGTGT  | CGTGTTTAAG  | 3600 |
| GACGGTCTCT  | AACAAGGAGG  | TCGTACAGGG  | AGATGGCCAA  | AGCAGACCGA  | GTTGCTGTAC  | 3660 |
| GCCCTTTTGG  | GAAAAATGCT  | AGGGTTGGTG  | GCAACGTTAC  | TAGGTCGACC  | AGAAGGCTTA  | 3720 |
| AGTCCTACCC  | CCCCCCCCCT  | TTTTTTTTTTT | TTTCCTCCAG  | AAGCCCTCTC  | TTGTCCCCGT  | 3780 |
| CACCGGGGGC  | ACCGTACATC  | TGAGGCCGAG  | AGGACGCGAT  | GGGCCCCGCT  | TCCAAGCCGG  | 3840 |
| TGTGGCTCGG  | CCAGCTGGCG  | CTTCGGGTCT  | TTTTTTTTTTT | TTTTTTTTTTT | TTTTCCTCCA  | 3900 |
| GAAGCCTTGT  | CTGTCTGTGT  | CACCGGGGGC  | GCTGTACTTC  | TGAGGCCGAG  | AGGACGCGAT  | 3960 |
| GGGCCCCGGC  | TTCCAAGCCG  | GTGTGGCTCG  | GCCAGCTGGA  | GCTTCGGGTC  | TTTTTTTTTTT | 4020 |
| TTTTTTTTTTT | TTTTTTTCTC  | CAGAAGCCTT  | GTCTGTCTGT  | GTCACCGGGG  | GCGCTGTACT  | 4080 |
| TCTGAGGCCG  | AGAGGACGCG  | ATGGGTCTGGC | TTCCAAGCCG  | ATGTGGCGGG  | GCCAGCTGGA  | 4140 |
| GCTTCGGGTT  | TTTTTTTTTTC | CTCCAGAAGC  | CCTCTCTTGT  | CCCCGTCACC  | GGGGGCGCTG  | 4200 |
| TACTTCTGAG  | GCCGAGAGGA  | CGTGATGGGC  | CCGGGTTCCA  | GCGGGATGTC  | GCCCGGTCAG  | 4260 |
| CTGGAGCTTT  | GGATCTTTTTT | TTTTTTTTTTT | CCTCCAGAAG  | CCCTCTCTTG  | TCCCCGTCAC  | 4320 |
| CGGGGGCACC  | TTACATCTGA  | GGGCGAGAGG  | ACGTGATGGG  | TCCGGCTTCC  | AAGCCGATGT  | 4380 |
| GGCGGGGCCA  | GCTGGAGCTT  | CGGGTTTTTTT | TTTTTTTCTC  | CAGAAGCCCT  | CTCTTGTCCC  | 4440 |
| CGTACCCGGG  | GCGCGTGATC  | TTCTGAGGCC  | GAGAGACGCT  | GATGGGCCCC  | GGTTTCCAGG  | 4500 |
| GGATGTCGCC  | CGGTACAGTG  | GAGCTTTGGA  | TCATTTTTTTT | TTTTCCCTCC  | AGAAGCCCTC  | 4560 |
| TCTTGTCCCC  | GTCACCGGGG  | GCACCGTACA  | TCTGAGGCCG  | AGAGGACACG  | ATGGGCCTGT  | 4620 |
| CTTCCAAGCC  | GATGTGGCCC  | GGCCAGCTGG  | AGCTTCGGGT  | CTTTTTTTTTT | TTTTTTCCTC  | 4680 |
| CAGAAGCCTT  | GTCTGTCTGT  | GTCACCCGGG  | GCGCTGTACT  | TCTGAGGCCG  | AGAGGACGCG  | 4740 |
| ATGGGCCCCG  | CTTCCAAGCC  | GGTGTGGCTC  | GGCCAGCTGG  | AGCTTCGGGT  | CTTTTTTTTTT | 4800 |
| TTTTTTTTTTT | TTCTCTCCAG  | AACCTTGTCT  | GTCTGTCTCA  | CCCGGGGCGC  | TTGTACTTCT  | 4860 |
| GATGCCGAGA  | GGACGCGATG  | GGCCCGTCTT  | CCAGGCCGAT  | GTGGCCCGGT  | CAGCTGGAGC  | 4920 |
| TTTGGATCTT  | TTTTTTTTTTT | TTTTCCTCCA  | GAAGCCCTCT  | CTTGTCCCCG  | TCACCGGGGG  | 4980 |
| CACCTTACAT  | CTGAGGCCAT  | GAGGACACGA  | TGGGCCCGGG  | TTCCAGGCCG  | ATGTGGCCCC  | 5040 |
| GTCAGCTGGA  | GCTTTGGATC  | TTTTTTTTTTT | TTTTCTTCCA  | GAAGCCCTCT  | TGTCCCCGTC  | 5100 |
| ACCGGTGGCA  | CTGTACATCT  | GAGGCGGAGA  | GGACATTATG  | GGCCCGGCTT  | CCAATCCGAT  | 5160 |
| GTGGCCCCGG  | CAGCTGGAGC  | TTTGGATCTT  | ATTTTTTTTTT | TAATTTTTTTC | TTCCAGAAGC  | 5220 |
| CCCTTTGTCC  | CTGTACCCGG  | TGGCACGGTA  | CATCTGAGGC  | CGAGAGGACA  | TTATGGGCCC  | 5280 |
| GCTCTTCCAG  | CCGATCTGGC  | CCGCTCTTGG  | GGAGCTTTGG  | ATCTTTTTTTT | TTTTTTTTTCT | 5340 |
| TTTTTCTCTC  | AGAAGCCCTC  | TCTGTCCCTG  | TCACCGGGGG  | CCCTGTACGT  | CTGAGGCCGA  | 5400 |
| GGGAAAGCTA  | TGGGCGCGGT  | TTTCTTTTCAT | TGACCTGTCTG | GTCTTATCAG  | TTCTCCGGGT  | 5460 |
| TGTACAGGTC  | GACCAAGTTGT | TCCTTTGAGG  | TCCGGTTCTT  | TTCTGTTATG  | GGTCATTTTTT | 5520 |
| GGGCCACCTC  | CCCAGGTATG  | ACTTCCAGGC  | GTCTGTCTCT  | GCCTGTCACT  | TTCTTCCCTG  | 5580 |
| TCTCTTTTAT  | GCTTGTGATC  | TTTCTATCTT  | GTTCCTATTG  | GACCTGGAGA  | TAGGTTAGTA  | 5640 |
| CACGCTGTCC  | TTTCCCTATT  | AACACTAAAG  | GACACTATAA  | AGAGACCCCT  | TCGATTTAAG  | 5700 |
| GCTGTTTTGC  | TTGTCCAGCC  | TATTCCTTTT  | ACTGGCTTGG  | GTCTGTCTCG  | GTGCCTGAAG  | 5760 |
| CTGTCCCCGA  | GCCACGCTTC  | CTGCTTTCCC  | GGGCTTGTCT  | CTTGGCTGTG  | CTTGTCTGTG  | 5820 |
| GCAGCTTTGT  | ACAACCTGGC  | GCTGTGACTT  | TGCTGCTGTG  | CAGACGTTTT  | TCCCATTCTC  | 5880 |
| CCCGAGGTGT  | GCTTGTACAC  | CCTGTCCCCT  | TTGGAATGGT  | GGAGCCAGCT  | GTGGTTGAGG  | 5940 |
| GCCACCTTAT  | TTCCGGCTCAC | TTTTTTTTTTT | TTTTTTTTTCT | TTGGAGTCCC  | GAACCTCCGC  | 6000 |
| TCTTTTCTCT  | TCCCCTGCTT  | TCTTCCACAT  | GCCTCCCAGG  | TGCATTTCTT  | TTTGTTTTTTT | 6060 |
| TTCTTTTTTTT | TTTTTTTTTTT | TTGGGGAGGT  | GGAGAGTCCC  | GAGTACTTCA  | CTCCTGTCTG  | 6120 |
| TGGTGTCCAA  | GTGTTTCATG  | CACGTGCCTC  | CCGAGTGCAC  | TTTTTTTTTGT | GGCAGTCTGT  | 6180 |
| CGTTGTGTTT  | TCTTGTCTGT  | TGTCTGCCCC  | TATCAGTAAC  | TGTCTTGTCC  | CGCGTGTAA   | 6240 |
| ACATTCCTAT  | CTCGCTTGT   | TCTCCCAGAT  | GCGCGTCTGT  | GCTCACTCTT  | AGATCGATGT  | 6300 |
| GGTGCTCCGG  | AGTTCTCTTC  | GGGCCAGGGC  | CAAGCCGCGC  | CAGGCGAGGG  | ACGGACATTC  | 6360 |
| ATGGCGAATG  | GCGGCCGCTC  | TTCTCGTTCT  | GCCAGCGGGC  | CCTCGTCTCT  | CCACCCCATC  | 6420 |
| CGTCTGCCGG  | TGGTGTGTGG  | AAGGCAGGGG  | TGCGGCTCTC  | CGGCCCGACG  | CTGCCCGCGC  | 6480 |
| CGCACTTTTC  | TCAGTGGTTC  | GCGTGGTCTT  | TGTGGATGTG  | TGAGGCGCCC  | GGTTGTGCCC  | 6540 |
| TCACGTGTTT  | CACTTTGGTC  | GTGTCTCGCT  | TGACCATGTT  | CCCAGAGTCG  | GTGGATGTGG  | 6600 |
| CCGGTGGCGT  | TGCATACCTT  | TCCCCTCTGG  | TGTGTGCACG  | CGCTGTTTCT  | TGTAAGCGTC  | 6660 |
| GAGGTGCTCC  | TGGAGCGTTC  | CAGGTTTGTG  | TCCTAGGTGC  | CTGCTTCTGA  | GCTGGTGGTG  | 6720 |
| GCGCTCCCCA  | TTCCCTGGTG  | TGCCCTCCGGT | GCTCCGCTCG  | GCTGTGTGCC  | TTCCCCGTTG  | 6780 |
| TGTCTGAGAA  | GCCCGTGAGA  | GGGGGGTCGA  | GGAGAGAAGG  | AGGGGCAAGA  | CCCCCTTCTT  | 6840 |
| TCGTGCGGTG  | AGGCGCCAC   | CCCGCGACTA  | GTACGCCTGT  | GCGTAGGGCT  | GGTGCTGAGC  | 6900 |
| GGTCGCGGCT  | GCGGTTGGAA  | AGTTTCTCGA  | GAGACTCATT  | GCTTTCCCGT  | GGGGAGCTTT  | 6960 |
| GAGAGGCTGT  | GCTTTCCGGG  | GGGACCGGTT  | GAGAGGCTCT  | CCCTGTCCGC  | GGATGCTCAG  | 7020 |
| AATGCCCTTG  | GAAGAGAACC  | TTCTTGTGTC  | CGCAGACCCC  | CCCGCGCGGT  | CGCCCCGCTG  | 7080 |

|             |             |             |            |             |             |       |
|-------------|-------------|-------------|------------|-------------|-------------|-------|
| TTGGTCTTCT  | GGTTTCCCTG  | TGTGCTCGTC  | GCATGCATCC | TCTCTCGGTG  | GCCGGGGGCTC | 7140  |
| GTCGGGGTTT  | TGGGTCCGTC  | CCGCCCTCAG  | TGAGAAAGTT | TCCTTCTCTA  | GCTATCTTCC  | 7200  |
| GGAAAGGGTG  | CGGGCTTCTT  | ACGGTCTCGA  | GGGGTCTCTC | CCGAATGGTC  | CCCTGGAGGG  | 7260  |
| CTCGCCCCCT  | GACCGCCTCC  | CGCGCGCGCA  | CGGTTTGGTC | TCTCGTCTAC  | CGCGGCCCCG  | 7320  |
| GGCCTCCCCG  | CTCCGAGTTC  | GGGGAGGGAT  | CACGCGGGGC | AGAGCCTGTC  | TGTCGTCTCTG | 7380  |
| CCGTTGCTGC  | GGAGCATGTG  | GCTCGGCTTG  | TGTGGTTGGT | GGCTGGGGAG  | AGGGCTCCGT  | 7440  |
| GCACACCCCC  | GCGTGCGCGT  | ACTTTCCTCC  | CCTCCTGAGG | GCCGCCGTGC  | GGACGGGGTG  | 7500  |
| TGGGTAGGCG  | ACGGTGGGCT  | CCCGGGTCCC  | CACCCGTCTT | CCCGTGCCCT  | ACCCGTGCCT  | 7560  |
| TCCGTGCGGT  | ACGTCCCTCT  | CGTCTCGGTC  | CACGACTTTG | GCCGCTCCCG  | CGACGGCGGC  | 7620  |
| CTGCGCCGCG  | CGTGGTGCCT  | GCTGTGTGCT  | TCTCGGGCTG | TGTGGTTGTG  | TCGCCTCGCC  | 7680  |
| CCCCCCTTCC  | CGCGGCAGCG  | TCCCCACGGC  | TGGCGAAATC | GCGGGAGTCC  | TCCTTCCCCCT | 7740  |
| CCTCGGGGTC  | GAGAGGGTCC  | GTGTCTGGCG  | TTGATTGATC | TCGCTCTCGG  | GGACGGGACC  | 7800  |
| GTTCTGTGGG  | AGAACGGCTG  | TTGGCCGCGT  | CCGGCGGAC  | GTCGGACGTG  | GGGACCCACT  | 7860  |
| GCCGCTCGGG  | GGTCTTCGTC  | GGTAGGCATC  | GGTGTGTGCG | CATCGGTCTC  | TCTCTCGTGT  | 7920  |
| CGGTGTGCGC  | TCCTCGGGCT  | CCCGGGGGGC  | CGTCGTGTTT | CGGGTCGGCT  | CGGCGCTGCA  | 7980  |
| GGTGTGGTGG  | GACTGCTCAG  | GGGAGTGGTG  | CAGTGTGATT | CCCGCCGGTT  | TTGCCTCGCG  | 8040  |
| TGCCCTGACC  | GGTCCGACGC  | CCGAGCGGTC  | TCTCGGTCCC | TTGTGAGGAC  | CCCCTTCCGG  | 8100  |
| GAGGGGCCCG  | TTTCGGCCCG  | CCTTGCCGTC  | GTCGCCGGCC | CTCGTTCTGC  | TGTGTCTGTT  | 8160  |
| CCCCCTCCCC  | GCTCGCCGCA  | GCCGGTCTTT  | TTTCTCTCT  | CCCCCCTCT   | CCTCTGACTG  | 8220  |
| ACCCGTGGCC  | GTGCTGTGCG  | ACCCCCCGCA  | TGGGGGCGGC | CGGGCACGTA  | CGCGTCCGGG  | 8280  |
| CGGTACCCGG  | GGTCTTGGGG  | GGGGGCCGAG  | GGGTAAGAAA | GTCGGCTCGG  | CGGGCGGGAG  | 8340  |
| GAGTCTGTGGT | TTGGAGGGCG  | TCCCGGCCCC  | CGCGGCTGG  | CGGTGTCTTG  | CGCGCCCTTG  | 8400  |
| GAGAGGGCTG  | GCTGCGAGGG  | GAAAAGGTTG  | CCCCGCGAGG | GCAAAGGGAA  | AGAGGCTAGC  | 8460  |
| AGTGGTCATT  | GTCCCGACGG  | TGTGGTGGTC  | TGTTGGCCGA | GGTGCCTCTG  | GGGGGCTCGT  | 8520  |
| CCGGCCCTGT  | CGTCCGTCGG  | GAAGGCGCGT  | GTTGGGGCCT | GCCGGAGTGC  | CGAGGTGGGT  | 8580  |
| ACCCTGGCGG  | TGGGATTAAC  | CCCGCGCGCG  | TGTCCCGGTG | TGGCGGTGGG  | GGCTCCGGTC  | 8640  |
| GATGTCTACC  | TCCCTCTCCC  | CGAGGTCTCA  | GGCCTTCTCC | CGCGGGGCTC  | TCGGCCCTCC  | 8700  |
| CCTCGTTCCT  | CCCTCTCGCG  | GGGTCTAAGT  | CGCTCGTCGA | CCTCCCTCC   | TCCGTCCTTC  | 8760  |
| CATCTCTCGC  | GCAATGGCGC  | CGCCCGAGTT  | CACGGTGGGT | TCGTCTCTCC  | CCTCCGCTTC  | 8820  |
| TCGCCGGGGG  | CTGGCCGCTG  | TCCGGTCTCT  | CCTGCCCGAC | CCCCGTGGC   | GTGGTCTTCT  | 8880  |
| CTCGCCGGCT  | TCGCGGACTC  | CTGGCTTCGC  | CCGGAGGGTC | AGGGGGCTTC  | CCGGTCCCC   | 8940  |
| GACGTTGCGC  | CTCGCTGCTG  | TGTGCTTGGG  | GGGGGCCCGC | TGCGGCCCTC  | CGCCGCCCGT  | 9000  |
| GAGCCCTGTC  | CGCACCCGCC  | GGTGTGCGGT  | TTGCGGCCGC | GGTCAGTTGG  | GCCCTGGCGT  | 9060  |
| TGTGTGCGGT  | CGGGAGCGTG  | TCCGCCTCGC  | GGCGGCTAGA | CGCGGGTGTC  | GCCGGGCTCC  | 9120  |
| GACGGGTGGC  | CTATCCAGGG  | CTCGCCCCCG  | CCGACCCCGC | CCTGCCCGTC  | CCGGTGGTGG  | 9180  |
| TCGTGGTGGT  | GGGGAGTGAA  | TGGTGTCTACC | TGTCATTCCC | TCCCGCGTGG  | TTTGACTGTC  | 9240  |
| TCGCCGGTGT  | CGCGCTTCTC  | TTTCCGCCAA  | CCCCACGCC  | AACCCACCAC  | CCTGCTCTCC  | 9300  |
| CGGCCCGGTG  | CGGTTCGACGT | TCCGGCTCTC  | CCGATGCCGA | GGGGTTCGGG  | ATTTGTGCCG  | 9360  |
| GGGACGGAGG  | GGAGAGCGGG  | TAAGAGAGGT  | GTCGGAGAGC | TGTCCCGGGG  | CGACGCTCGG  | 9420  |
| GTTGGCTTTG  | CCGCGTGCCT  | GTGCTCGCGG  | ACGGGTTTTG | TCGGACCCCG  | ACGGGGTCCG  | 9480  |
| TCCGGCCGCA  | TGCACTCTCC  | CGTTCGCGCG  | CAGCGCCCGC | CCGGCTCACC  | CCCGCTTTGT  | 9540  |
| CCTCCCGCGA  | GGCTCTCCGC  | CGCCGCCGCC  | TCCTCCTCCT | CTCTCGCGCT  | CTCTGTCCCG  | 9600  |
| CCTGGTCCTG  | TCCCACCCCC  | GACGCTCCGC  | TCGCGCTTCC | TTACCTGGTT  | GATCCTGCCA  | 9660  |
| GGTAGCATAT  | GCTTGTCTCA  | AAGATTAAGC  | CATGCATGTC | TAAGTACGCA  | CGGCCGGTAC  | 9720  |
| AGTGAAGTCT  | CGAATGGCTC  | ATTAAATCAG  | TTATGGTTCC | TTTGGTCTGCT | CGCTCCTCTC  | 9780  |
| CTACTTGGAT  | AACTGTGGTA  | ATTCTAGAGC  | TAATACATGC | CGACGGGCGC  | TGACCCCTCT  | 9840  |
| TCCCGGGGGG  | GGATGCGTGC  | ATTTATCAGA  | TCAAAACCAA | CCCGGTGAGC  | TCCCTCCCGG  | 9900  |
| CTCCGGCCCG  | GGGTCCGGCG  | CCGGCGGCTT  | GGTGACTCTA | GATAACCTCG  | GGCCGATCGC  | 9960  |
| ACGCCCCCCC  | TGGCGGCGAC  | GACCCATTCC  | AACGTCTGCC | CTATCAACTT  | TCGATGGTAG  | 10020 |
| TCGCCGTGCC  | TACCATGGTG  | ACCACGGGTG  | ACGGGGAATC | AGGGTTCGAT  | TCCGGAGAGG  | 10080 |
| GAGCCTGAGA  | AACGGCTACC  | ACATCCAAGG  | AAGGCAGCAG | GCGCGCAAAT  | TACCCACTCC  | 10140 |
| CGACCCGGGG  | AGGTAGTGAC  | GAAAAATAAC  | AATACAGGAC | TCTTTCGAGG  | CCCTGTAATT  | 10200 |
| GGAATGAGTC  | CACTTTAAAT  | CCTTTAACGA  | GGATCCATTG | GAGGGCAAAGT | CTGGTGCCAG  | 10260 |
| CAGCCGCGGT  | AATTCCAGCT  | CCAATAGCGT  | ATATTAAAGT | TGCTGCAGTT  | AAAAAGCTCG  | 10320 |
| TAGTTGGATC  | TTGGGAGCGG  | GCGGGCGGTC  | CGCCGCGAGG | CGAGTCACCG  | CCCGTCCCCG  | 10380 |
| CCCCCTGCTT  | CTCGGCGCCC  | CCTCGATGCT  | CTTAGCTGAG | TGTCCCGCGG  | GGCCCGAAGC  | 10440 |
| GTTTACTTTG  | AAAAAATTAG  | AGTGTTCAAA  | GCAGGCCCGA | GCCGCCCTGGA | TACCGCAGCT  | 10500 |
| AGGAATAATG  | GAATAGGACC  | GCGGTTCTAT  | TTTGTTGGTT | TTCGGAACTG  | AGGCCATGAT  | 10560 |
| TAAGAGGGAC  | GGCCGGGGGC  | ATTCGTATTG  | CGCCGCTAGA | GGTGAAATTC  | TTGGACCGGC  | 10620 |
| GCAAGACGGA  | CCAGAGCGAA  | AGCATTTGCC  | AAGCATGTTT | TCATTAAATC  | AGAACGAAAG  | 10680 |
| TCGGAGGTTT  | GAAGACGATC  | AGATACCGTC  | GTAGTTCCGA | CCATAAACGA  | TGCCGACTGG  | 10740 |
| CGATGCGGCG  | GCGTTATTCC  | CATGACCCGC  | CGGGCAGCTT | CCGGGAAACC  | AAAGTCTTTG  | 10800 |
| GGTTCCGGGG  | GGAGTATGGT  | TGCAAAGCTG  | AAACTTAAAG | GAATTGACGG  | AAGGGCACCA  | 10860 |
| CCAGGAGTGG  | GCCTGCGGCT  | TAATTTGACT  | CAACACGGGA | AACCTCACCC  | GGCCCGGACA  | 10920 |
| CGACAGGAT   | TGACAGATTG  | ATAGCTCTTT  | CTCGATTCCG | TGGGTGGTGG  | TGCATGGCCG  | 10980 |

|             |            |             |            |             |             |       |
|-------------|------------|-------------|------------|-------------|-------------|-------|
| TTCTTAGTTG  | GTGGAGCGAT | TTGTCTGGTT  | AATTCCGATA | ACGAACGAGA  | CTCTGGCATG  | 11040 |
| CTAACTAGTT  | ACGCGACCCC | CGAGCGGTCTG | GCGTCCCCCA | ACTTCTTAGA  | GGGACAAGTG  | 11100 |
| GCGTTTCAGCC | ACCCGAGATT | GAGCAATAAC  | AGGTCTGTGA | TGCCCTTAGA  | TGTCGCGGGC  | 11160 |
| TGCACGCGCG  | CTACACTGAC | TGGCTCAGCG  | TGTGCCTACC | CTGCGCCGGC  | AGGCGCGGGT  | 11220 |
| AACCCGTTGA  | ACCCCATTCG | TGATGGGGAT  | CGGGGATTGC | AATTATTCCT  | CATGAACGAG  | 11280 |
| GAATTCCTCAG | TAAGTGCGGG | TCATAAGCTT  | GCGTTGATTA | AGTCCCTGCC  | CTTTGTACAC  | 11340 |
| ACCGCCCGTC  | GCTACTACCG | ATTGGATGGT  | TTAGTGAGGC | CCTCGGATCG  | GCCCCGCCGG  | 11400 |
| GGTCGGCCCA  | CGGCCCTGGC | GGAGCGCTGA  | GAAGACGGTC | GAACCTTGACT | ATCTAGAGGA  | 11460 |
| AGTAAAGTC   | GTAACAAGGT | TTCCGTAGGT  | GAACCTGCGG | AAGGATCATT  | AAACGGGAGA  | 11520 |
| CTGTGGAGGA  | GCGGCGGCGT | GGCCCGCTCT  | CCCCGTCTTG | TGTGTGTCCT  | CGCCGGGAGG  | 11580 |
| CGCGTGCCTG  | CCGGGTCCCG | TCGCCCGCGT  | GTGGAGCGAG | GTGTCTGGAG  | TGAGGTGAGA  | 11640 |
| GAAAGGGTGG  | GTGGGGTCCG | TCTGGGTCCG  | TCTGGGACCG | CCTCCGATTT  | CCCCTCCCC   | 11700 |
| TACCCCTCTCC | CTCGTCCGGC | TCTGACCTCG  | CCACCTTACC | GCGGCGGCGG  | CTGCTCGCGG  | 11760 |
| GCGTCTTGCC  | TCTTTCCCGT | CCGGCTCTTC  | CGTGTCTACG | AGGGGCGGTA  | CGTCTGTTACG | 11820 |
| GGTTTTTGAC  | CCGTCCCGGG | GGCGTTCGGT  | CGTCGGGGCG | CGCGCTTTGC  | TCTCCCGGCA  | 11880 |
| CCCATCCCCG  | CCGCGGCTCT | GGCTTTTCTA  | CGTTGGCTGG | GGCGGTTGTC  | GCGTGTGGGG  | 11940 |
| GGATGTGAGT  | GTCGCGTGTG | GGTCTGCCCC  | TCCCGATGCC | ACGCTTTTCT  | GGCCTCGCGT  | 12000 |
| GTCCCTCCCCG | CTCCTGTCCC | GGGTACCTAG  | CTGTGCGGTT | CCGGCGCGGA  | GGTTTAAGGA  | 12060 |
| CCCCGGGGGG  | GTCGCCCTGC | CGCCCCCAGG  | GTCGGGGGGC | GGTGGGGCCC  | GTAGGGAAGT  | 12120 |
| CGGTGCTTCG  | GGCGGCTCTC | CCTCAGACTC  | CATGACCCTC | CTCCCCCCCC  | TGCCCGCCGT  | 12180 |
| CCCCGAGGCG  | CGGTGCTGTG | GGGGGTGGA   | TGTCTGGAGC | CCCCTCGGGC  | GCCGTGGGGG  | 12240 |
| CCCCAGCCCG  | CGCGCCGGCT | TGCCCGATTT  | CGCGGGTTCG | GTCCGTGTCG  | TGCCGTGCGT  | 12300 |
| GGGTTCCTCGT | GTCGTTCCCG | TGTTTTTCCG  | CTCCCGACCC | TTTTTTTTTTC | CTCCCCCCCCA | 12360 |
| CACGTGTCTC  | GTTTCGTTCC | TGCTGGCCCG  | CCTGAGGCTA | CCCCTCGGTC  | CATCTGTTCT  | 12420 |
| CCTCTCTCTC  | CGGGGAGAGG | AGGGCGGTGG  | TCGTTGGGGG | ACTGTGCCGT  | CGTCAGCACC  | 12480 |
| CGTGAGTTCC  | CTCACACCCG | AAATACCGAT  | ACGACTCTTA | GCGGTGGATC  | ACTCGGCTCG  | 12540 |
| TGCGTCGATG  | AAGAACGCAG | CTAGCTGCGA  | GAATTAATGT | GAATTGCAGG  | ACACATTGAT  | 12600 |
| CATCGACACT  | TCGAACGCAC | TTGCGGCCCC  | GGGTTCCTCC | CGGGGCTACG  | CCTGTCTGAG  | 12660 |
| CGTCGGTTGA  | CGATCAATCG | CGTCACCCGC  | TGCGGTGGGT | GCTGCGCGGC  | TGGGAGTTTG  | 12720 |
| CTCGCAGGGC  | CAACCCCCCA | ACCCGGGTCCG | GGCTCTCCGT | CTCCCGAAGT  | TCAGACGTGT  | 12780 |
| GGGCGGTTGT  | CGGTGTGGCG | CGCGCGCCCG  | CGCTCGCGAG | CCTGGTCTCC  | CCCGCGCATC  | 12840 |
| CGCGCTCGCG  | GCTTCTTCCC | GCTCCGCCGT  | TCCCGCCCTC | GCCCGTGAC   | CCCGGTCTTG  | 12900 |
| GCCTCGCGTC  | GGCGCCTCCC | GGACCGCTGC  | CTCACCAGTC | TTTCTCGGTC  | CCGTGCCCCG  | 12960 |
| TGGGAACCCA  | CCGCGCCCCC | GTGGCGCCCG  | GGGGTGGGCG | CGTCCGCATC  | TGCTCTGGTC  | 13020 |
| GAGGTGTGGCG | GTTGAGGGTG | TGCGTGCCGC  | GAGGTGGTGG | TCCGTCCCCC  | GCGGCGCGCG  | 13080 |
| GGTTGTCCGG  | GTGGCGGTCG | ACGAGGGCCG  | CTCGGTCCGC | TGCGGTGGTT  | GTCTGTGTGT  | 13140 |
| GTTTGGGTCT  | TGCGCTGGGG | GAGGCGGGGT  | CGACCGCTCG | CGGGGTGGGC  | GCGGTGCCCC  | 13200 |
| GGCGCCGCGC  | ACCCTCCGGC | TTGTGTGGAG  | GGAGAGCGAG | GGCGAGAACG  | GAGAGAGGTG  | 13260 |
| GTATCCCCGG  | TGGCGTTGCG | AGGGAGGGTT  | TGGCGTCCCG | CGTCCGTCCG  | TCCCTCCCTC  | 13320 |
| CCTCGGTGGG  | CGCCTTCGCG | CCGCACGCGC  | CCGCTAGGGG | CGGTCGGGGC  | CCGTGGCCCC  | 13380 |
| CGTGGCTCTT  | CTTCGTCTCC | GCTTCTCCTT  | CACCCGGGCG | GTACCCGCTC  | CGGCGCCGGC  | 13440 |
| CCGCGGGACG  | CCGCGGCGTC | CGTGCGCCGA  | TGCGAGTCAC | CCCCGGGTGT  | TGCGAGTTCTG | 13500 |
| GGGAGGGAGA  | GGGCCTCGCT | GACCCGTTGC  | GTCCCGGCTT | CCCTGGGGGG  | GACCCGGCGT  | 13560 |
| CTGTGGGCTG  | TGCGTCCCGG | GGGTTGCGTG  | TGAGTAAGAT | CCTCCACCCC  | CGCCGCCCTC  | 13620 |
| CCCTCCCGCG  | GGCCTCTCGG | GGACCCCTTG  | AGACGGTTCT | CCGGCTCGTC  | CTCCGCTGCC  | 13680 |
| GCCGGGTGCC  | GTCTCTTTCC | CGCCCGCCTC  | CTCGCTCTCT | TCTTCCCGCG  | GCTGGGCGCG  | 13740 |
| TGTCCCCCTT  | TTCTGACCGC | GACCTCAGAT  | CAGACGTGGC | GACCCGCTGA  | ATTTAAGCAT  | 13800 |
| ATTAGTCAGC  | GGAGGAAAAG | AAACTAACCA  | GGATTCCCTC | AGTAACGGCG  | AGTGAACAGG  | 13860 |
| GAAGAGCCCA  | GCGCCGAATC | CCCGCCGCGC  | GTGCGGGCGT | GGGAAATGTG  | GCGTACGGAA  | 13920 |
| GACCCACTCC  | CCGGCGCCCG | TGCTGGGGGG  | CCCAAGTCCT | TCTGATCGAG  | GCCCAGCCCG  | 13980 |
| TGGACGGTGT  | GAGGCCGGTA | GCGGCCCGCG  | CGCGCCGGGC | TCGGGTCTTC  | CCGGAGTCGG  | 14040 |
| GTTGCTTGGG  | AATGCAGCCC | AAAGCGGGTG  | GTAAACTCCA | TCTAAGGCTA  | AATACGGGCA  | 14100 |
| CGAGACCGAT  | AGTCAACAAG | TACCGTAAGG  | GAAAGTTGAA | AAGAACTTTG  | AAGAGAGAGT  | 14160 |
| TCAAGAGGGC  | GTGAAACCGT | TAAGAGGTAA  | ACGGGTGGGG | TCCGCGCAGT  | CCGCCCGGAG  | 14220 |
| GATTCAACCC  | GGCGGCGCGC | GTCCGGCCGT  | GCCCAGTGGT | CCCGGCGGAT  | CTTTCCCGCT  | 14280 |
| CCCCGTTCTT  | CCCGACCCCT | CCACCCGCGC  | GTCGTTCCCC | TCTTCTCTCC  | CGCGTCCGGC  | 14340 |
| GCCTCCGGCG  | GCGGGCGCGG | GGGGTGGTGT  | GGTGGTGGCG | CGCGGGCGGG  | GCCGGGGGTG  | 14400 |
| GGGTCCGGCG  | GGGACCGCCC | CCGGCCGGCG  | ACCGGCCCGC | GCCGGGCGCA  | CTTCCACCGT  | 14460 |
| GGCGGTGCGC  | CGCGACCGCG | TCCGGGACCG  | CCGGGAAGGC | CCGGTGGGGA  | AGGTGGCTCG  | 14520 |
| GGGGGGGCGG  | CGCGTCTCAG | GGCGCGCCGA  | ACCACCTCAC | CCCGAGTGT   | ACAGCCCTCC  | 14580 |
| GGCCGCGCTT  | TCGCCGAATC | CCGGGGCCGA  | GGAAGCCAGA | TACCCGTCGC  | CGCGCTCTCC  | 14640 |
| CTCTCCCCCC  | GTCCGCCTCC | CGGGCGGGCG  | TGGGGGTGGG | GGCCGGGCGG  | CCCCTCCCAC  | 14700 |
| GGCGCGACCG  | CTCTCCACAC | CCCCTCCGTC  | GCCTCTCTCG | GGGCCCCGGT  | GGGGGCGGGG  | 14760 |
| CGGACTGTCC  | CCAGTGCGCC | CCGGGCGTCG  | TCGCGCCGTC | GGGTCCCGGG  | GGGACCGTCG  | 14820 |
| GTCACGCGTC  | TCCCCAGCAA | GCCGAGCGCA  | CGGGGTCCGC | GGCGATGTCC  | GCTACCCACC  | 14880 |

|            |             |             |            |            |            |       |
|------------|-------------|-------------|------------|------------|------------|-------|
| CGACCCGTCT | TGAAACACGG  | ACCAAGGAGT  | CTAACGCGTG | CGCGAGTCAG | GGGCTCGTCC | 14940 |
| GAAAGCCGCC | GTGGCGCAAT  | GAAGGTGAAG  | GGCCCCGCC  | GGGGGCCCGA | GGTGGGATCC | 15000 |
| CGAGGCCTCT | CCAGTCCGCC  | GAGGGCGCAC  | CACCGGCCCG | TCTCGCCCGC | CGCGCCGGGG | 15060 |
| AGGTGGAGCA | CGAGCGTACG  | CGTTAGGACC  | CGAAAGATGG | TGAACATATG | TTGGGCAGGG | 15120 |
| CGAAGCCAGA | GGAAACTCTG  | GTGGAGGTCC  | GTAGCGGTCC | TGACGTGCAA | ATCGGTCTGT | 15180 |
| CGACCTGGGT | ATAGGGGCGA  | AAGACTAATC  | GAACCATCTA | GTAGCTGGTT | CCCTCCGAAG | 15240 |
| TTTCCCTCAG | GATAGCTGGC  | GCTCTCGCTC  | CCGACGTACG | CAGTTTTATC | CGGTAAAGCG | 15300 |
| AATGATTAGA | GGTCTTGGGG  | CCGAAACGAT  | CTCAACCTAT | TCTCAAACCT | TAAATGGGTA | 15360 |
| AGAAGCCCGG | CTCGCTGGCG  | TGGAGCCGGG  | CGTGGAAATG | GAGTGCCTAG | TGGGCCACTT | 15420 |
| TTGGTAAGCA | GAAGTGGCGC  | TGCGGGATGA  | ACCGAACGCC | GGGTTAAGGC | GCCCGATGCC | 15480 |
| GACGCTCATC | AGACCCAGAG  | AAAGGTGTTG  | GTTGATATAG | ACAGCAGGAC | GGTGGCCATG | 15540 |
| GAAGTCGGAA | TCCGCTAAGG  | AGTGTGTAAC  | AACTCACCTG | CCGAATCAAC | TAGCCCTGAA | 15600 |
| AATGGATGGC | GCTGGAGCGT  | CGGGCCCATG  | CCCGGCCGTC | GCCGCAGTCG | GAACGGAACG | 15660 |
| GGACGGGAGC | GGCCGCGGGT  | GCGCGTCTCT  | CGGGGTGCGG | GGTGCCTGGC | GGGGGCCCGT | 15720 |
| CCCCCGCCTC | CCCTCCGCGC  | GCCGGGTTCG  | CCCCCGCGGC | GTCGGGCCCC | GCGGAGCCTA | 15780 |
| CGCCGCGACG | AGTAGGAGGG  | CCGCTGCGGT  | GAGCCTTGAA | GCCTAGGGCG | CGGGCCCGGG | 15840 |
| TGGAGCCGCC | GCAGGTGCAG  | ATCTTGGTGG  | TAGTAGCAAA | TATTCAAACG | AGAACTTTGA | 15900 |
| AGGCCGAAGT | GGAGAAGGGT  | TCCATGTGAA  | CAGCAGTTGA | ACATGGGTCA | GTCCGTCTCT | 15960 |
| AGAGATGGGC | GAGTGCCGTT  | CCGAAGGGAC  | GGGCGATGGC | CTCCGTTGCC | CTCGGCCGAT | 16020 |
| CGAAAGGGAG | TGGGTTTCAG  | ATCCCGAAT   | CCGAGTGGC  | GGAGATGGGC | GCCGCGAGGC | 16080 |
| CAGTGCGGTA | ACGCGACCGA  | TCCCGGAGAA  | GCCGCGGGGA | GGCTCGGGG  | AGAGTTCTCT | 16140 |
| TTTCTTTGTG | AAGGCGAGGG  | GCCTCTGAA   | TGGGTTGCGC | CCGAGAGAGG | GGCGGTCGCC | 16200 |
| TTGGAAAGCG | TCCGCGTTCC  | GCGCGCTCTC  | GCTGAGCTCT | CGCTGGCCCT | TGAAATCCG  | 16260 |
| GGGGAGAGGG | TGTAAATCTC  | GCGCCGGGCC  | GTACCCATAT | CCGCAGCAGG | TCTCCAAGGT | 16320 |
| GAACAGCCTC | TGGCATGTTG  | GAACAATGTA  | GGTAAGGGAA | GTCGGCAAGC | CGGATCCGTA | 16380 |
| ACTTCGGGAT | AAGGATTGGC  | TCTAAGGGCT  | GGGTGCGTCG | GGCTGGGGCG | CGAAGCGGGG | 16440 |
| CTGGGCGCGC | GCCGCGGCTG  | GACGAGGCGC  | GCCCGCCCTC | TCCCACGTCC | GGGGAGACCC | 16500 |
| CCCGTCCTTT | CCGCCCCGGC  | CCGCCCTCCC  | CTCTTCCCCG | CGGGGCCCCG | TCGTCCCCCG | 16560 |
| CGTCGTCGCC | ACCTCTCTTC  | CCCCCTCCTT  | CTTCCCGTCG | GGGGGCGGGT | CGGGGGTCGG | 16620 |
| CGCGCGGCGC | GGGCTCCGGG  | GCGGCGGGTC  | CAACCCCGCG | GGGGTTCCGG | AGCGGGAGGA | 16680 |
| ACCAGCGGTC | CCCGGTGGGG  | CGGGGGGGCC  | GGACACTCGG | GGGGCCGGCG | GCGCGGCGGA | 16740 |
| CTCTGGAGCG | GAGCCGGGCC  | CTTCCCGTGG  | ATCGCCTCAG | CTGCGGCGGG | CTGCGGCGCC | 16800 |
| GCTCCCGGGG | AGCCCGGCGG  | GTGCCGGCGC  | GGGTCCCCTC | CCCGCGGGGC | CTCGCTCCAC | 16860 |
| CCCCCATCG  | CCTCTCCCGA  | GGTGCGTGGC  | GGGGGCGGGC | GGGCGTGTCC | CGCGCGTGTG | 16920 |
| GGGGGAACCT | CCGCGTCGGT  | GTTCCCCCGC  | CGGGTCCGCC | CCCCGGGCCG | CGGTTTTCCG | 16980 |
| CGCGGCGGCC | CCGCCTCGGC  | CGCGCCTAG   | CAGCCGACTT | AGAACTGGTG | CGGACCAGGG | 17040 |
| GAATCCGACT | GTTTAAATTAA | AACAAAGCAT  | CGCGAAGGCC | CGCGGCGGGT | GTTGACGCGA | 17100 |
| TGTGATTTCT | GCCCAGTGCT  | CTGAATGTCA  | AAGTGAAGAA | ATTCAATGAA | GCGCGGGTAA | 17160 |
| ACGGCGGGAG | TAACATATGAC | TCTCTTAAAG  | TAGCCAAATG | CCTCGTCATC | TAATTAGTGA | 17220 |
| CGCGCATGAA | TGGATGAACG  | AGATTCCCAC  | TGTCCCTACC | TACTATCCAG | CGAAACCACA | 17280 |
| GCCAAGGGAA | CGGGCTTGGC  | GGAATCAGCG  | GGAAATAAAG | ACCCTGTTGA | GCTTGACTCT | 17340 |
| AGTCTGGCAC | GGTGAAGAGA  | CATGAGAGGT  | GTAGAATAAG | TGGGAGGCCC | CCGGCGCCCC | 17400 |
| GCCCCGTCTT | CGCGTCGGGG  | TCGGGGCAGC  | CCGGCCTCGC | GGGCCGCCCG | TGAAATACCA | 17460 |
| CTACTCTCAT | CGTTTTTTTCA | CTGACCCGGT  | GAGGCGGGGG | GGCGAGCCCC | GAGGGGCTCT | 17520 |
| CGCTTCTGGC | GCCAAGCGTC  | CGTCCCGCGC  | TGCGGGCGCG | GCGCGACCCG | CTCCGGGGAC | 17580 |
| AGTGCCAGGT | GGGGAGTTTG  | ACTGGGGCGG  | TACACCTGTC | AAACGGTAAC | GCAGGTGTCC | 17640 |
| TAAGGCGAGC | TCAGGGAGGA  | CAGAAACCTC  | CCGTGGAGCA | GAAGGGCAAA | AGCTCGCTTG | 17700 |
| ATCTTGATTT | TCAGTACGAA  | TACAGACCGT  | GAAAGCGGGG | CCTCACGATC | CTTCTGACCT | 17760 |
| TTTGGGTTTT | AAGCAGGAGT  | TGTCAGAAAA  | GTTACCACAG | GGATAACTGG | CTTGTGGCGG | 17820 |
| CAAAGCGTTC | ATAGCGACGT  | CGCTTTTTTGA | TCCTTCGATG | TCGGCTCTTC | CTATCATTTG | 17880 |
| GAAGCAGAAT | TCACCAAGCG  | TTGGATTGTT  | CACCCACTAA | TAGGGAACGT | GAGCTGGGTT | 17940 |
| TAGACCGTCG | TGAGACAGGT  | TAGTTTTACC  | CTACTGATGA | TGTGTTGTTG | CCATGGTAAT | 18000 |
| CCTGCTCAGT | ACGAGAGGAA  | CCGCAGGTTT  | AGACATTTGG | TGTATGTGCT | TGGCTGAGGA | 18060 |
| GCCAATGGGG | CGAAGCTACC  | ATCTGTGGGA  | TTATGACTGA | ACGCCTCTAA | GTCAGAATCC | 18120 |
| GCCCCAAGCG | AACGATACGG  | CAGCGCCGAA  | GGAGCCTCGG | TTGGCCCCCG | ATAGCCGGGT | 18180 |
| CCCCGTCCGT | CCCGCTCGGC  | GGGGTCCCCG  | CGTCGCCCCG | CGGCGGCGCG | GGGTCTCCCC | 18240 |
| CCGCCGGGGC | TGGGACCGGG  | GGTCCGGTGC  | GGAGAGCCGT | TCGTCTTGGG | AAACGGGGTG | 18300 |
| CGGCCGGAAA | GGGGGCCGCC  | CTCTCGCCCC  | TCACGTTGAA | CGCACGTTCC | TGTGGAACCT | 18360 |
| GGCGCTAAAC | CATTCTGATA  | CGACCTGCTT  | GTTTCTGTCG | GTTTCTGTCG | TAGCAGAGCA | 18420 |
| GCTCCCTCGC | TGCGATCTAT  | TGAAAGTCAG  | CCCTCGACAC | AAGGGTTTGT | CTCTGCGGGC | 18480 |
| TTTCCCGTCG | CACGCCCGCT  | CGCTCGCACG  | CGACCGTGTC | GCCGCCCGGG | CGTCACGGGG | 18540 |
| GCGGTGCGCT | CGGCCCCCGC  | GCGGTTGCCC  | GAACGACCGT | GTGGTGGTTG | GGGGGGGGAT | 18600 |
| CGTCTTCTCC | TCCGTCTCCC  | GAGGACGGTT  | CGTTTCTCTT | TCCCCTTCCG | TCGCTCTCCT | 18660 |
| TGGGTGTGGG | AGCCTCGTGC  | CGTCGCGACC  | GCGGCTGCCC | GTCGCTGCCC | GCCGCGGCCG | 18720 |
| CTTGCCCTCC | GGCCTTGGCC  | AAGCCGGAGG  | GCGGAGGAGG | GGGATCGGCG | GCGGCGGCGA | 18780 |



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 GCCGGGGGGG CGCTCTCTCC GCCCGAGCAT CCCCCTCCC GCCCCTCCTC TTCGCGCGCC 18960  
 GCGGCGGCGA CGTGCGTACG AGGGGAGGAT GTCGCGGTGT GGAGGCGGAG AGGGTCCGGC 19020  
 GCGGCGCCTC TTCCATTTT TCCCCCCCAA CTTGCGAGGT CGACCAGTAC TCCGGGCGAC 19080  
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 TACTTATAAT AATAGGTCGC CCGGTGGTGG TAGCTTCCCG GACTCCAGAG GCAGAGGCAG 20280  
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 AATAGATAGA TGGATAGAGT GATACAAATA TAGGTTTTTT TTTTCAAGTAA TATGAGGTTG 20520  
 ATTAACCACT TTTCCCTTTT TAGGTTTTTT TTTTTTTCCC CTGTCCATGT GGTGCTGGG 20580  
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 TCTGTAGACC AGCCTGGCCT CAATCGAACT CAGAAATCCT CCTGCCCTCT GTCTACCTCC 20820  
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 TGTTCTCACT CTGCCACCAA CGCGCTTTGT ACATTGAATG TGAGCTTTGT TTTGCTTAAC 21420  
 AGACATATAT TTTTCTTTT GGTTTTGCTT GACATGGTTT CCCTTTCTAT CCGTGCAGGG 21480  
 TTCCCAGACG GCCTTTTGAG AATAAAATGG GAGGCCAGAA CCAAAGTCTT TTGAATAAAG 21540  
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 GGAAAAGCAT GTAGCAGTTG TAGGACACAC TAGACGAGAG CACCAGATCT CATTGTGGGT 21660  
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 ATGGCCTGGT TCTCTGAAC GTTGAGCCTT GTCTATCCAG AGGCTGACTG GCTAGTTTTT 22080  
 TACCTGAAGT CCCTGAGTGA TGATTTCCCT GTGAATTC 22118

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42999 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| GCTGACACGC | TGTCCTCTGG | CGACCTGTCTG | TCGGAGAGGT | TGGGCCTCCG | GATGCGCGCG | 60   |
| GGGCTCTGGC | CTCACGGTGA | CCGGCTAGCC  | GGCCGCGCTC | CTGCCTTGAG | CCGCCTGCCG | 120  |
| CGGCCCGCGG | GCCTGCTGTT | CTCTCGCGCG  | TCCGAGCGTC | CCGACTCCCG | GTGCCGGCCC | 180  |
| GGGTCCGGGT | CTCTGACCCA | CCCGGGGGCG  | GCGGGGAAGG | CGGCGAGGGC | CACCGTGCCC | 240  |
| CGTGCGCTCT | CCGCTGCGGG | CGCCCGGGGC  | GCCGCACAAC | CCCACCCGCT | GGCTCCGTGC | 300  |
| CGTGCGGTGC | AGGCGTTCTC | GTCTCCGCGG  | GGTTGTCCGC | CGCCCCTTCC | CCGGAGTGGG | 360  |
| GGGTGGCCGG | AGCCGATCGG | CTCGCTGGCC  | GGCCGGCCTC | CGCTCCCGGG | GGGCTCTTCG | 420  |
| ATCGATGTGG | TGACGTCTGT | CTCTCCCGGG  | CCGGGTCCGA | GCCGCGACGG | GCGAGGGGCG | 480  |
| GACGTTTCGT | GCGAACGGGA | CCGTCTTTCT  | CGCTCCGCCC | GCGCGGTCCC | CTCGTCTGCT | 540  |
| CCTCTCCCCG | CCCGCCGGCC | GGCGTGTGGG  | AAGGCGTGGG | GTGCGGACCC | CGGCCCGACC | 600  |
| TCGCCGTCCC | GCCCCCGGCC | TTCGCTTCGC  | GGGTGCGGGC | CGGCGGGGTC | CTCTGACGCG | 660  |
| GCAGACAGCC | CTGCCTGTCT | CCTCCAGTGG  | TTGTGCACTT | GCGGGCGGCC | CCCCTCCGCG | 720  |
| GCGGTGGGGG | TGCCGTCCCG | CCGGCCCGTC  | GTGCTGCCCT | CTCGGGGGGG | GTTTGCGCGA | 780  |
| GCGTTCGGTC | CGCTGGGGCC | CTTGCGGTGC  | TCCTGGAGCG | CTCCGGGTTG | TCCCTCAGGT | 840  |
| GCCCGAGGCC | GAACGGTGGT | GTGTCTGTTT  | CGCCCCCGGC | GCCCCCTCCT | CCGGTCGCCG | 900  |
| CCGCGGTGTC | CGCGCGTGGG | TCCTGAGGGA  | GCTCGTCCGT | GTGGGGTTTC | AGGCGGTTTG | 960  |
| AGTGAGACGA | GACGAGACGC | GCCCCCTCCA  | CGCGGGGAAG | GGCGCCCGCC | TGCTCTCGGT | 1020 |
| GAGCGCACGT | CCCGTGCTCC | CCTCTGGCGG  | GTGCGCGCGG | GCCGTGTGAG | CGATCGCGGT | 1080 |
| GGGTTCCGGC | CGGTGTGACG | CGTGCGCCGG  | CCGGCCCGCG | AGGGGCTGCC | GTTCTGCCTC | 1140 |
| CGACCGGTTC | TGTGTGGGTT | GACTTCGGAG  | GCGCTCTGCC | TCGGAAGGAA | GGAGGTGGGT | 1200 |
| GGACGGGGGG | GCCTGGTGGG | GTTGCGCGCA  | CGCGCGCACC | GGCCGGGCCC | CCGCCCTGAA | 1260 |
| CGCGAACGCT | CGAGGTGGCC | GCGCGCAGGT  | GTTTCCTCGT | ACCGCAGGGC | CCCCTCCCTT | 1320 |
| CCCCAGGCGT | CCCTCGGCGC | CTCTGCGGGC  | CCGAGGAGGA | GCGGCTGGCG | GGTGGGGGGA | 1380 |
| GTGTGACCCA | CCCTCGGTGA | GAAAAGCCTT  | CTCTAGCGAT | CTGAGAGGCG | TGCCTTGGGG | 1440 |
| GTACCGGATC | CCCCGGGCCG | CCGCCTCTGT  | CTCTGCCTCC | GTTATGGTAG | CGCTGCCGTA | 1500 |
| GCGACCCGCT | CGCAGAGGAC | CCTCCTCCGC  | TTCCCCCTCG | ACGGGGTTGG | GGGGGAGAAG | 1560 |
| CGAGGGTTCC | GCCGGCCACC | GCGGTGGTGG  | CCGAGTGCGG | CTCGTCGCCT | ACTGTGGCCC | 1620 |
| GCGCCTCCCC | CTTCCGAGTC | GGGGGAGGAT  | CCCCCGGGGC | CGGGCCCGGC | GCTCCCACCC | 1680 |
| AGCGGGTTGG | GACGCGGCGG | CCGCGGGGCG  | GTGGGTGTGC | GCGCCCGGCG | CTCTGTCCGG | 1740 |
| CGCGTGACCC | CCTCCGTCCG | CGAGTCGGCT  | CTCCGCCCCG | TCCCGTGCCG | AGTCGTGACC | 1800 |
| GGTGCCGACG | ACCGCGTTTG | CGTGGCACGG  | GGTCGGGCCC | GCCTGGCCCT | GGGAAAGCGT | 1860 |
| CCCACGGTGG | GGGCGCGCCG | GTCTCCCGGA  | CGGGGACCGG | GTGCGAGGAT | GGACGAGAAT | 1920 |
| CACGAGCGAC | GGTGGTGGTG | GCGTGTGGTG  | TTCTAGCGAT | CGGTGCGTCC | GGGGCCCCCG | 1980 |
| GTGGCGGGGC | CCCGGGGCTC | GCGAGGCGGT  | TCTCGGTGGG | GGCCGAGGGC | CGTCCGGCGT | 2040 |
| CCCAGGCGGG | GCGCCGCGGG | ACCGCCCTCG  | TGTCTGTGGC | GGTGGGATCC | CGCGGCCGTG | 2100 |
| TTTTCTCTGG | GGCCCGGGCG | TGCCTGAGGT  | TTCTCCCCGA | GCCGCCGCCT | CTGCGGGCTC | 2160 |
| CCGGGTGCCC | TTGCCCTCGC | GGTCCCCGGC  | CCTCGCCCCG | CTGTGCCCTC | TTCCCCGCCC | 2220 |
| GCCGCCCGCC | GATCCTCTTC | TTCCCCCGCA  | CGGGCTCACG | GGCTTCACGT | CCGTTGTTGG | 2280 |
| CCCCGCCTGG | GACCGAACCC | GGCACCGCCT  | CGTGGGGCGC | CGCCGCCGGC | CACTGATCGG | 2340 |
| CCCGGCGTCC | GCGTCCCCCG | GCGCGCGCCT  | TGGGGACCGG | GTGCGGTGGC | CGCCGCGTGG | 2400 |
| GGCCCGGTGG | GCTTCCCGGA | GGGTTCGCGG  | GGTCGGCCTG | CGGCGCGTGC | GGGGGAGGAG | 2460 |
| ACGGTTCCGG | GGGACCGGCC | GCGGCTGCGG  | CGGCGGCGGT | GGTGGGGGGA | GCCGCGGGGA | 2520 |
| TCGCCGAGGG | CCGGTCGGCC | GCCCCGGGTG  | CCCCCGGGTG | CCGCCGGCGG | CGGTGAGGCC | 2580 |
| CCGCGCGTGT | GTCCCGGCTG | CGGTGCGGCC  | CGCTCAGAGG | GTCCCCGTGG | CGTCCCCCTC | 2640 |
| CCCGCCGGCC | GCCTTTCTCG | CGCCTTCCCC  | GTGCCCCCGG | CCTCGCCCGT | GGTCTCTCGT | 2700 |
| CTTCTCCCGG | CCCGCTCTTC | CGAACCGGGT  | CGGCGCGTCC | CCCGGGTGCG | CCTCGCTTCC | 2760 |
| CGGGCCTGCC | GCGGCCCTTC | CCCGAGGCGT  | CCGTCCCGGG | CGTCGGCGTC | GGGAGAGACC | 2820 |
| CGTCTCCCCC | GCGTGGCGTC | GCCCCGTTCC  | GCGCGCGCGT | GCGCCCGAGC | GCGGCCCGGT | 2880 |
| GGTCCCTCCC | GGACAGGCGT | TCGTGCGACG  | TGTGGCGTGG | GTGACCTTCC | GCCTTGCCGG | 2940 |
| TCGCTCGCCC | TCTCCCCGGG | TCGGGGGGTG  | GGGCCCCGGC | CGGGGCCTCG | GCCCCGGTCG | 3000 |
| CTGCTTCCCG | TCCCGGGCGG | GGGCGGGGCG  | GCCGGCCGGC | CTCGGTGCGC | CTCCCTTGCG | 3060 |
| CGTCTGTGGG | CGTGTGCCAC | CCCTGCGCCG  | GCGCCCGCGG | GCGGGGCTCG | GAGCGGGGCT | 3120 |
| TCGGCCGGGC | CCCGGGCCCT | CGACCGGACC  | GGCTGCGCGG | GCGCTGCGGC | GCGACGGCGC | 3180 |
| GACTGTCCCC | GGGCCGGGCA | CCGCGGTCCG  | CCTCTCGCTC | GCCGCCCGGA | CGTCGGGGCC | 3240 |
| GCCCCGCGGG | GCGGGCGGAG | CGCCGTCCCC  | GCCTCGCCGC | CGCCCGCGGG | CGCCGGCCCG | 3300 |
| GCGCGCGCGC | GCGTGGCCGC | CGGTCCCTCC  | CGGCCGCGCG | GCGCGGGTCG | GGCCGTCCGC | 3360 |
| CTCCTCGCGG | GCGGAAGCGA | TCGCGGGTCT  | GTGGCGCGGG | GCCCCGGGTG | 3420       |      |



|             |            |            |            |             |             |      |
|-------------|------------|------------|------------|-------------|-------------|------|
| GTCGTGTCGC  | GTGGGGGGCG | GGTGGTTGGG | GCGTCCGGTT | CGCCGCGCCC  | CGCCCCGGCC  | 3480 |
| CCACCGGTCC  | CGGCCGCCGC | CCCCGCGCCC | GCTCGCTCCC | TCCCGTCCGC  | CCGTCCGCGG  | 3540 |
| CCCGTCCGTC  | CGTCCGTCCG | TCGTCTCTCT | CGCTTGCGGG | GCGCCGGGGC  | CGTCTCTGCG  | 3600 |
| AGGCCCCCG   | GCCGGCCGTC | CGGCCGCGTC | GGGGGCTCGC | CGCGCTCTAC  | CTTACCTACC  | 3660 |
| TGGTTGATCC  | TGCCAGTAGC | ATATGCTTGT | CTCAAAGATT | AAGCCATGCA  | TGTCTAAGTA  | 3720 |
| CGCACGGCCG  | GTACAGTGAA | ACTGCGAATG | GCTCATTAAG | TCAGTTATGG  | TTCTTTTGGT  | 3780 |
| CGCTCGCTCC  | TCTCTACTTT | GGATAACTGT | GGTAATTCTA | GAGCTAATAC  | ATGCCGACGG  | 3840 |
| GCGCTGACCC  | CCTTCGCGGG | GGGGATGCGT | GCATTTATCA | GATCAAAACC  | AACCCGGTCA  | 3900 |
| GCCCCCTCTC  | GGCCCCGGCC | GGGGGGCGGG | CGCCGGCGGC | TTTGGTGACT  | CTAGATAACC  | 3960 |
| TCGGGGCCGAT | CGCACGCCCC | CCGTGGCGGC | GACGACCCAT | TCGAACGTCT  | GCCCTATCAA  | 4020 |
| CTTTTCGATGG | TAGTCGCCGT | GCCTACCATG | GTGACCACGG | GTGACGGGGA  | ATCAGGGTTC  | 4080 |
| GATTCCGGAG  | AGGGAGCCTG | AGAAACGGGT | ACCACATCCA | AGGAAGGCAG  | CAGGCGCGCA  | 4140 |
| AATTACCCAC  | TCCCAGCCCG | GGGAGGTAGT | GACGAAAAAT | AACAATACAG  | GACTCTTTTC  | 4200 |
| AGGCCCTGTA  | ATTGGAATGA | GTCCACTTTA | AATCCTTTAA | CGAGGATCCA  | TTGGAGGGCA  | 4260 |
| AGTCTGGTGC  | CAGCAGCCGC | GGTAATTCCA | GCTCCAATAG | CGTATATTAA  | AGTTGCTGCA  | 4320 |
| GTTAAAAAGC  | TCGTAGTTGG | ATCTTGGGAG | CGGGCGGGCG | GTCCGCCGCG  | AGGCGAGCCA  | 4380 |
| CGCCCCGTCC  | CCGCCCCCTT | CCTCTCGGGC | CCCCCTCGAT | GCTCTTAGCT  | GAGTGTCCCG  | 4440 |
| CGGGGCCCGA  | AGCGTTTACT | TTGAAAAAAT | TAGAGTGTTT | AAAGCAGGCC  | CGAGCCGCCT  | 4500 |
| GGATACCGCA  | GCTAGGAATA | ATGGAATAGG | ACCGCGGTTT | TATTTTGTGT  | GTTTTCGGAA  | 4560 |
| CTGAGGCCAT  | GATTAAGAGG | GACGGCCGGG | GGCATTCGTA | TTGCGCCGCT  | AGAGGTGAAA  | 4620 |
| TTCTTGGACC  | GGCGCAAGAC | GGACCAGAGC | GAAAGCATTT | GCCAAGAATG  | TTTTTCATTAA | 4680 |
| TCAAGAACGA  | AAGTCGGAGG | TTGGAAGACG | ATCAGATACC | GTCGTAGTTC  | CGACCATAAA  | 4740 |
| CGATGCCGAC  | CGGGCATGCG | GCGGCGTTAT | TCCCATGACC | CGCCGGGCGA  | CTTCCGGGAA  | 4800 |
| ACCAAAGTCT  | TTGGGTTCGG | GGGGGAGTAT | GGTTGCAAAG | CTGAAACTTA  | AAGGAATTGA  | 4860 |
| CGGAAGGGCA  | CCACCAGGAG | TGGAGCCTGC | GGCTTAATTT | GACTCAACAC  | GGGAAACCTC  | 4920 |
| ACCCGGCCCC  | GACACGGACA | GGATTGACAG | ATTGATAGCT | CTTTCTCGAT  | TCCGTGGGTG  | 4980 |
| GTGGTGCATG  | GCGGTCTTAA | GTGGTGGAG  | CGATTTGTCT | GGTTAATTCC  | GATAACGAAC  | 5040 |
| GAGACTCTGG  | CATGCTAACT | AGTTACGCGA | CCCCCGAGCG | GTCGGCGTCC  | CCCAACTTCT  | 5100 |
| TAGAGGGACA  | AGTGGCGTTC | AGCCACCCGA | GATTGAGCAA | TAACAGGTCT  | GTGATGCCCT  | 5160 |
| TAGATGTCCG  | GGGCTGCACG | CGCGCTACAC | TGACTGGCTC | AGCGTGTGCC  | TACCCTACGC  | 5220 |
| CGGCAGGCGC  | GGGTAACCCG | TTGAACCCCA | TTCGTGATGG | GGATCGGGGA  | TTGCAATTAT  | 5280 |
| TCCCCATGAA  | CGAGGGAATT | CCCAGTAAAG | TGCGGGTCAT | AAGCTTGCGT  | TGATTAAGTC  | 5340 |
| CCTGCCCTTT  | GTACACACCG | CCCGTCGCTA | CTACCGATTG | GATGGTTTAG  | TGAGGCCCTC  | 5400 |
| GGATCGGCCC  | CGCCGGGGTC | GGCCACGCGC | CCTGGCGGAG | CGCTGAGAAG  | ACGGTCAAC   | 5460 |
| TTGACTATCT  | AGAGGAAGTA | AAAGTCGTAA | CAAGGTTTCC | GTAGGTGAAC  | CTGCGGAAGG  | 5520 |
| ATCATTAAAC  | GAGCCCCGAG | GGCGAGGCCC | GCGGCGCGCG | CGCCGCCGCC  | GCGCGCTTCC  | 5580 |
| CTCCGACAC   | CCACCCCGCC | ACCGCGACGC | GCGCGGTGCG | CGGGCGGGGC  | CCGCGTGCCC  | 5640 |
| GTTCGTTTCG  | TCGCTCGTTC | GTTCCGCCGC | CGGCCCGGCC | GCCGCGAGAG  | CCGAGAACTC  | 5700 |
| GGGAGGGAGA  | CGGGGGGGAG | AGAGAGAGAG | AGAGAGAGAG | AGAGAGAGAG  | AGAGAGAGAA  | 5760 |
| AGAAGGGCGT  | GTCGTTGGTG | TGCGCGTGTC | GTGGGGCGCG | CGGGCGGGCG  | GGAGCGGTCC  | 5820 |
| CGGGCGCGCG  | CCCCGACGAC | GTGGGTGTCT | GCGGGCGCGG | GGGCGGTTCT  | CGGCGGCGTC  | 5880 |
| GCGGCGGGTC  | TGGGGGGGTC | TCGGTGCCCT | CCTCCCCGCC | GGGGCCCCGTC | GTCCGGCCCC  | 5940 |
| GCCGCGCCCG  | CTCCCCGTCT | TCGGGGCCCG | CCGGATTCCC | GTCGCCCTCC  | CCGCGCCGCT  | 6000 |
| CCGCGCCGCC  | GGGACCGGCC | CCGCTCGCTC | TCCCCGGCCT | TCCCCGCTAGG | GCGTCTCGAG  | 6060 |
| GGTCGGGGGC  | CGGACCGCGG | TCCCCCTCCC | CGCCTCTCTG | TCCGCCCCCC  | CGCCGTCCAG  | 6120 |
| GTACCTAGCG  | CGTTCCGGCG | CGGAGGTTTA | AAGACCCTCT | GGGGGGGATCG | CCCGTCCGCG  | 6180 |
| CGTGGGTTCG  | GGGCGGTGGT | GGGCCCGCGG | GGGAGTCCCG | TCGGGAGGGG  | CCCGGCCCTC  | 6240 |
| CCCGCGCCTC  | CACCGCGGAC | TCCGCTCCCC | GGCCGGGGCC | GCGCCGCCGC  | CGCCGCCGCG  | 6300 |
| GCGGCCGTGC  | GGTGGGGGCT | TTACCCGGCG | GCCGTGCGCG | GCCTGCCGCG  | CGTGTGGCGT  | 6360 |
| GCGCCCCGCG  | CCGTGGGGGC | GGGAACCCCC | GGGCGCCTGT | GGGGTGGTGT  | CCGCGCTCGC  | 6420 |
| CCCCGCGTGG  | GCGGCGCGCG | CCTCCCCGTG | GTGTGAAACC | TTCCGACCCC  | TCTCCGGAGT  | 6480 |
| CCGGTCCCGT  | TTGCTGTCTC | GTCTGGCCCG | CCTGAGGCAA | CCCCCTCTCC  | TCTTGGGCGG  | 6540 |
| GGGGGGCGGG  | GGGACGTGCC | GCGCCAGGAA | GGGCCTCCTC | CCGGTGCGTC  | GTCGGGAGCG  | 6600 |
| CCCTCGCCAA  | ATCGACCTCG | TACGACTCTT | AGCGGTGGAT | CACTCGGCTC  | GTGCGTCGAT  | 6660 |
| GAAGAACGCA  | GCTAGCTGCG | AGAATTAATG | TGAATTGCAG | GACACATTGA  | TCATCGACAC  | 6720 |
| TTCGAACGCA  | CTTGCGGGCC | CGGGTTCCCT | CCGGGGCTAC | GCCTGTCTGA  | GCGTCGCTTG  | 6780 |
| CCGATCAATC  | GCCCCGGGGG | TGCCTCCGGG | CTCCTCGGGG | TGCGCGGCTG  | GGGGTTCCCT  | 6840 |
| CGCAGGGCCC  | GCCGGGGGGC | CTCCGTCCCC | CTAAGCGCAG | ACCCGGCGGC  | GTCCGCCCTC  | 6900 |
| CTCTTGCCCG  | CGGCCCCGCC | CCTTCCCCCT | CCCCCGCGCG | GCCCTGCGTG  | GTCACGCGTC  | 6960 |
| GGGTGGCGGG  | GGGGAGAGGG | GGGCGCGCCC | GCGTCGAGAG | GACGGGGAGG  | GCGGCGCGCG  | 7020 |
| CGCCGGAAGA  | CGGAGAGGGA | AAGAGAGAGC | CGGCTCGGGC | CGAGTTCCCG  | TGGCCGCCGC  | 7080 |
| CTGCGGTCCG  | GGTTCTCTCC | TCGGGGGGCT | CCCTCGCGCC | GCGCGCGGCT  | CGGGGTTCCG  | 7140 |
| GGTTCGTCCG  | CCCCGGCCCG | GTGGAAGGTC | CCGTGCCCGT | CGTCTGCTGC  | GTCGCGCGTC  | 7200 |
| GTCGGCGGTG  | GGGGCGTGTT | GCGTGCGGTG | TGGTGGTGGG | GGAGGAGGAA  | GGCGGGTCCG  | 7260 |
| GAAGGGGAAG  | GGTGCCGGCG | GGGAGAGAGG | GTCGGGGGAG | CGCGTCCCGG  | TCGCGCGGTT  | 7320 |

|            |            |            |            |             |             |       |
|------------|------------|------------|------------|-------------|-------------|-------|
| TCCGCCGCCC | GCCCCCGGTG | GCGGCCCGGC | GTCCGGCCGA | CCGGCCGCTC  | CCCGCGCCCC  | 7380  |
| TCCTCCTCCC | CGCCGCCCTT | CCTCCGAGGC | CCCGCCCGTC | CTCCTCGCCC  | TCCCCGCGCG  | 7440  |
| TACGCGCGCG | CGCCCGCCCG | CCCGGCTCGC | CTCGCGGCGC | GTGCGCCGGG  | GCCGGGAGCC  | 7500  |
| CGCCCCGCGG | CCCGCCCGTG | GCCGCGGCGC | CGGGGTTCGC | GTGTCCCCCG  | CGGCGACCCG  | 7560  |
| CGGGACGCGG | CGGTGTCGTC | CGCCGTCGCG | CGCCCGCCTC | CGGCTCGCGG  | CCGCGCCGCG  | 7620  |
| CCGCGCCGGG | GCCCCGTCCC | GAGCTTCCGC | GTGCGGGCGG | CGCGGCTCCG  | CCGCCGCGTC  | 7680  |
| CTCGGACCCG | TCCCCCCGAC | CTCCGCGGGG | GAGACGCGCC | GGGGCGTGCG  | GCGCCCGTCC  | 7740  |
| CGCCCCCGGC | CCGTGCCCTT | CCCTCCGGTC | GTCCCGCTCC | GGCGGGGCGG  | CGCGGGGCGG  | 7800  |
| CCGTGCGGCG | CGCGCTCTCT | CTCCCGTCGC | CTCTCCCCCT | CGCCGGGCCC  | GTCTCCCGAC  | 7860  |
| GGAGCGTCGG | GCGGGCGGTC | GGGCGGCGCG | GATTCCGTCC | GTCCGTCCGC  | CGAGCGGCCC  | 7920  |
| GTCCCCCTCC | GAGACGCGAC | CTCAGATCAG | ACGTGGCGAC | CCGCTGAATT  | TAAGCATATT  | 7980  |
| AGTCAGCGGA | GGAAAAGAAA | CTAACAGGA  | TTCCCTCAGT | AACGGCGAGT  | GAACAGGGAA  | 8040  |
| GAGCCGAGCG | CCGAATCCCC | GCCCGCGGGG | GCGCGGAGCA | TGTGGCGTAC  | GGAAAGACCCG | 8100  |
| CTCCCCGGCG | CCGCTCGTGG | GGGGCCCAAG | TCCTTCTGAT | CGAGGCCCCAG | CCCGTGGACG  | 8160  |
| GTGTGAGGCC | GGTAGCGGCC | GGCGCGCGCC | CGGGTCTTCC | CGGAGTCGGG  | TTGCTTGGGA  | 8220  |
| ATGCAGCCCA | AAGCGGGTGG | TAAACTCCAT | CTAAGGCTAA | ATACCGGCAC  | GAGACCGATA  | 8280  |
| GTCAACAAGT | ACCGTAAGGG | AAAGTTGAAA | AGAACTTTGA | AGAGAGAGTT  | CAAGAGGGCG  | 8340  |
| TGAAACCGTT | AAGAGGTAAA | CGGGTGGGGT | CCGCGCAGTC | CGCCCGGAGG  | ATTCAACCCG  | 8400  |
| GCGGCGGGTC | CGGCCGTGTC | GGCGGCCCGG | CGGATCTTTC | CCGCCCCCCG  | TTCCTCCCGA  | 8460  |
| CCCCTCCACC | CGCCCTCCCT | TCCCCCGCCG | CCCCTCCTCC | TCCTCCCCCG  | AGGGGGCGGG  | 8520  |
| CTCCGGCGGG | TGCGGGGGTG | GGCGGGCGGG | GCCGGGGGTG | GGGTGCGCGG  | GGGACCGTCC  | 8580  |
| CCCGACCGGC | GACCGGCCGC | CGCCGGGCGC | ATTTCCACCG | CGGCGGTGCG  | CCGCGACCCG  | 8640  |
| CTCCGGGACG | GTCGGGAAGG | CCCGCGGGGG | CCCGGCGCTC | GGGGGGCCCC  | GTCCGTCCGT  | 8700  |
| CCGTCTCTCT | CCTCCCCCGT | CTCCGCCCCC | CGGCCCCGCG | TCCTCCCTCG  | GGAGGGCGCG  | 8760  |
| CGGGTCGGGG | CGGCGGCGGC | GGCGGCGGTG | GCGGCGGCGG | CGGGGGCGGC  | GGGACCGAAA  | 8820  |
| CCCCCCCCGA | GTGTTACAGC | CCCCCGGCA  | GCAGACTCGC | CCGAATCCCG  | GGGCGGAGGG  | 8880  |
| AGCGAAGCCC | GTCGCCCGCG | TCTCCCCCTT | CCCGGCGCCC | ACCCCGCGCG  | GGAATCCCCC  | 8940  |
| GCGAGGGGGG | TCTCCCCCGC | GGGGGCGCGC | CGGCGTCTCC | TCGTGGGGGG  | GCCGGGCCAC  | 9000  |
| CCCTCCCACG | GCGCGACCGC | TCTCCCACCC | CTCTTCCCCG | CGCCCCCGCC  | CCGGCGACGG  | 9060  |
| GGGGGGTGCC | GCGCGCGGGT | CGGGGGGCGG | GGCGGACTGT | CCCCAGTGCG  | CCCCGGGCGG  | 9120  |
| GTGCGGCCGT | CGGGCCCGGG | GGAGGTTCTC | TCGGGGCCAC | GCGCGCGTCC  | CCCGAAGAGG  | 9180  |
| GGGACGGCGG | AGCGAGCGCA | CGGGGTCGGC | GCGCAGCTCG | GCTACCCACC  | GCTACCCGTC  | 9240  |
| TGAAACACGG | ACCAAGGAGT | CTAACACGTG | CGCGAGTCGG | GGGCTCGCAC  | GAAAGCCGCC  | 9300  |
| GTGGCGCAAT | GAAGGTGAAG | GCCGCGCGCG | TCGCCGGCCG | AGGTGGGATC  | CCGAGGCCTC  | 9360  |
| TCCAGTCCGC | CGAGGGCGCA | CCACCGGCCC | GTCTCGCCCC | CCGCGCCGGG  | GAGGTGGAGC  | 9420  |
| ACGAGCGCAC | GTGTTAGGAC | CCGAAAGATG | GTGAACTATG | CCTGGGCAGG  | GCGAAGCCAG  | 9480  |
| AGGAAACTCT | CGTGGAGGTC | CGTAGCGGTC | CTGACGTGCA | AATCGGTCGT  | CCGACCTGGG  | 9540  |
| TATAGGGGCG | AAAGACTAAT | CGAACCATCT | AGTAGCTGGT | TCCCTCCGAA  | GTTTCCCTCA  | 9600  |
| GGATAGCTGG | CGCTCTCGCA | GACCCGACGC | ACCCCGGCCA | CGCAGTTTTC  | TCCGTTAAAG  | 9660  |
| CGAATGATTA | GAGGTCTTGG | GGCCGAAACG | ATCTCAACCT | ATTCTCAAAC  | TTTAAATGGG  | 9720  |
| TAAGAAGCCC | GGCTCGCTGG | CGTGGAGCCG | GCGGTGGAAT | GCGAGTGCCT  | AGTGGGCCAC  | 9780  |
| TTTTGGTAAG | CAGAACTGGC | GCTGCGGGAT | GAACCGAACG | CCGGGTAAAG  | GCGCCCGATG  | 9840  |
| CCGACGCTCA | TCAGACCCCA | GAAAAGGTGT | TGGTTGATAT | AGACAGCAGG  | ACGGTGGCCA  | 9900  |
| TGGAAGTCGG | AATCCGCTAA | GGAGTGTGTA | ACAACCTACC | TGCCGAATCA  | ACTAGCCCTG  | 9960  |
| AAAATGGATG | GCGCTGGAGC | GTCGGGCCCC | TACCCGGCCG | TCGCCGGCAG  | TCGAGAGTGG  | 10020 |
| ACGGGAGCGG | CGGGGGCGGC | GCGCGCGCGC | GCCGCTGTGG | TGTGCGTCCG  | AGGGCGGCGG  | 10080 |
| CGGCGGCGGC | GGCGGGGGTG | TGGGGTCCCT | CCCCCGCCCC | CCCCCCCACG  | CCTCTTCCCC  | 10140 |
| TCCTCCCGCC | CACGCCCCGC | TCCCCGCCCC | CGGAGCCCCG | CGGACGCTAC  | GCCGCGACGA  | 10200 |
| GTAGGAGGGC | CGCTGCGGTG | AGCCTTGAAG | CCTAGGGCGC | GGGCCCCGGT  | GGAGCCGCCG  | 10260 |
| CAGGTGCAGA | CTTTGGTGGT | AGTAGCAAAT | ATTCAAACGA | GAACCTTGAA  | GGCCGAAGTG  | 10320 |
| GAGAAGGGTT | CCATGTGAAC | AGCAGTTGAA | CATGGGTGAG | TCGGTCTCTGA | GAGATGGGCG  | 10380 |
| AGCGCCGTTT | CGAAGGGACG | GGCGATGGCC | TCCGTTGCCC | TCGGCCGATC  | GAAAGGGAGT  | 10440 |
| CGGGTTCAGA | TCCCCGAATC | CGGAGTGGCG | GAGATGGGCG | CCGCGAGGCG  | TCCAGTGCGG  | 10500 |
| TAACGCGACC | GATCCCGGAG | AAGCCGGCGG | GAGCCCCGGG | GAGAGTTCTC  | TTTTCTTTGT  | 10560 |
| GAAGGGCAGG | GCGCCCTGGA | ATGGGTTGCG | CCCAGAGAGG | GGGCCCCGTC  | CTTGGAAGAG  | 10620 |
| GTCGCGGTTT | CGGCGGCGTC | CGGTGAGCTC | TCGCTGGCCC | TTGAAAATCC  | GGGGGAGAGG  | 10680 |
| GTGTAAATCT | CGCGCCGGGC | CGTACCCATA | TCCGCAGCAG | GTCTCCAAGG  | TGAACAGCCT  | 10740 |
| CTGGCATGTT | GGAACAATGT | AGGTAAAGGA | AGTCGGCAAG | CCGGATCCGT  | AACTTCGGGA  | 10800 |
| TAAGGATTGG | CTCTAAGGGC | TGGGTCGGTC | GGGCTGGGGC | GCGAAGCGGG  | GCTGGGCGCG  | 10860 |
| CGCCGCGGCT | GCGCAGGCGC | GCGCCCCCCC | CCACGCCCGG | GGCAGCCCCC  | TGCGGCCCCC  | 10920 |
| CCCCCGCCCC | ACCCGCGCGC | GCCGCTCGCT | CCCTCCCCAC | CCCGCGCCCT  | CTCTCTCTCT  | 10980 |
| CTCTCCCCCG | CTCCCCGTCC | TCCCCCTTCC | CCGGGGGAGC | GCCGCGTGGG  | GGCGCGGCGG  | 11040 |
| GGGGAGAAGG | GTCGGGGCGG | CAGGGGCGCG | GCGGCGGCGG | CCGGGGGCGG  | CGGCGGGGGC  | 11100 |
| AGGTCCCCCG | GAGGGGGGCC | CCGGGGACCC | GGGGGGCCGG | CGGCGGCGCG  | GACTCTGGAC  | 11160 |
| GCGAGCCGGG | CCCTTCCCGT | GGATCGCCCC | AGCTGCGGCG | GCGTTCGCGG  | CCGCCCCCGG  | 11220 |

|             |             |            |             |             |             |       |
|-------------|-------------|------------|-------------|-------------|-------------|-------|
| GGAGCCCCGGC | GGCGGCGCGG  | CGCGCCCCCC | ACCCCCACCC  | CACGTCTCGG  | TCGCGCGCGC  | 11280 |
| GTCCGCTGGG  | GGCGGGAGCG  | GTCGGGCGGC | GGCGGTGCGC  | GGGCGGCGGG  | GCGGGGCGGT  | 11340 |
| TCGTCCCCCC  | GCCCTACCCC  | CCCGGCCCGG | TCCGCCCCCC  | GTTCCCCCCT  | CCTCCTCGGC  | 11400 |
| GCGCGGCGGC  | GGCGGCGGCA  | GGCGGCGGAG | GGGCGGCGGG  | CCGCTCCCCC  | CCGCCGGGTC  | 11460 |
| CGCCCCCGGG  | GCCGCGGTTC  | CGCGCGCGCC | TCGCTCGGC   | CGGCGCCTAG  | CAGCCGACTT  | 11520 |
| AGAAGTGGTG  | CGGACCAGGG  | GAATCCGACT | GTTTAATTAA  | AACAAAGCAT  | CGCGAAGGCC  | 11580 |
| CGCGGCGGGT  | GTTGACGCGA  | TGTGATTTCT | GCCCAGTGCT  | CTGAATGTCA  | AAGTGAAGAA  | 11640 |
| ATTCAATGAA  | GCGCGGGTAA  | ACGGCGGGAG | TAACATAGAC  | TCTCTTAAGG  | TAGCCAAATG  | 11700 |
| CCTCGTCATC  | TAATTAGTGA  | CGCGCATGAA | TGGATGAACG  | AGATTCCCAC  | TGTCCCTACC  | 11760 |
| TACTATCCAG  | CGAAACCACA  | GCCAAGGGAA | CGGGCTTGCC  | GGAATCAGCG  | GGGAAAGAAG  | 11820 |
| ACCCTGTTGA  | GCTTGACTCT  | AGTCTGGCAC | GGTGAAGAGA  | CATGAGAGGT  | GTAGAATAAG  | 11880 |
| TGGGAGGCCC  | CCGGCGCCCC  | CCCGGTGTCC | CCGCGAGGGG  | CCCGGGGCGG  | GGTCCGCGGC  | 11940 |
| CCTGCGGGCC  | GCCGCTGAAA  | TACCACTACT | CTGATCGTTT  | TTTCACTGAC  | CCGGTGAGGC  | 12000 |
| GGGGGGGCGA  | GCCCCGAGGG  | CTCTCGCTTC | TGGCGCCAAG  | CGCCCCGCCG  | GCCGGGCGCG  | 12060 |
| ACCCGCTCCG  | GGGACAGTGC  | CAGGTGGGGA | GTTTGACTGG  | GGCGGTACAC  | CTGTCAAACG  | 12120 |
| GTAACGCAGG  | TGTCCTAAGG  | CGAGCTCAGG | GAGGACAGAA  | ACCTCCCCTG  | GAGCAGAAGG  | 12180 |
| GCAAAAGCTC  | GCTTGATCTT  | GATTTTCAGT | ACGAATACAG  | ACCGTGAAAG  | CGGGGCCTCA  | 12240 |
| CGATCCTTCT  | GACCTTTTGG  | GTTTTAAGCA | GGAGGTGTCA  | GAAAAGTTAC  | CACAGGGATA  | 12300 |
| ACTGGCTTGT  | GGCGGCCAAG  | CGTTCATAGC | GACGTCGCTT  | TTTGATCCTT  | CGATGTCGGC  | 12360 |
| TCTTCCTATC  | ATTGTGAAGC  | AGAATTCGCC | AAGCGTTGGA  | TTGTTACACC  | ACTAATAGGG  | 12420 |
| AACGTGAGCT  | GGGTTTAGAC  | CGTCGTGAGA | CAGGTTAGTT  | TTACCCCTACT | GATGATGTGT  | 12480 |
| TGTTGCCATG  | GTAATCCTGC  | TCAGTACGAG | AGGAACCGCA  | GGTTCAGACA  | TTTGGTGTAT  | 12540 |
| GTGCTTGGCT  | GAGGAGCCAA  | TGGGGCGAAG | CTACCATCTG  | TGGGATTATG  | ACTGAACGCC  | 12600 |
| TCTAAGTCAG  | AATCCCGCCC  | AGGCGAACGA | TACGGCAGCG  | CCGCGGAGCC  | TCGGTTGGCC  | 12660 |
| TCGGATAGCC  | GGTCCCCCGC  | CTGTCCCCCG | CGGCGGGCCG  | CCCCCCCCCTC | CACGCGCCCC  | 12720 |
| GCCGCGGGAG  | GGCGCGTGCC  | CCGCCGCGCG | CCGGGACCGG  | GGTCCGGTGC  | GGAGTGCCCT  | 12780 |
| TCGTCTGGG   | AAACGGGGCG  | CGGCCGGAAG | GGCGGCCGCC  | CCCTCGCCCC  | TCACGCACCG  | 12840 |
| CACGTTTCGTG | GGGAACCTGG  | CGCTAAACCA | TTCTAGACAG  | ACCTGCTTCT  | GGGTGCGGGT  | 12900 |
| TTCGTACGTA  | GCAGAGCAGC  | TCCCTCGCTG | CGATCTATTG  | AAAGTCAGCC  | CTCGACACAA  | 12960 |
| GGGTTTGTCC  | GCGCGCGCGT  | GCGTGCGGGG | GGCCCCGCGG  | GCGTGCGCGT  | TCGGCGCCCT  | 13020 |
| CCGTCTTCTC  | GTTTCGTCTC  | CTCCCTCCCC | GCCTCTCCCC  | CCGACCGCGG  | CGTGGTGGTG  | 13080 |
| GGGTGGGGGG  | GAGGGCGCGG  | GACCCCGGTC | GGCCGCCCCG  | CTTCTTCGGT  | TCCCGCCTCC  | 13140 |
| TCCCCGTTCA  | CGCCGGGGCG  | GCTCGTCCGC | TCCGGGCCGG  | GACGGGGTCC  | GGGGAGCGTG  | 13200 |
| GTTTGGGAGC  | CGCGGAGGCG  | CCGCGCCGAG | CCGGGCCCCG  | TGGCCCGCCG  | GTCCCGCTCC  | 13260 |
| CGGGGGTTGG  | CCGCGCGGCG  | CGGTGGGGGG | CCACCCGGGG  | TCCCGGCCCT  | CGCGCGTCTC  | 13320 |
| TCCTCTCTCG  | TCCTCCGCAC  | GGTTCGACCG | ACGAACCGCG  | GGTGGCGGGC  | GGCGGGCGGC  | 13380 |
| GAGCCCCACG  | GGCGTCCCCG  | CACCCGGCCG | ACCTCCGCTC  | GCGACCTCTC  | CTCGGTGCGG  | 13440 |
| CCTCCGGGGT  | CGACCGCCTG  | CGCCCGCGGG | CGTGAGACTC  | AGCGGCGTCT  | CGCCGTGTCC  | 13500 |
| CGGGTCGACC  | GCGGCCTTCT  | CCACCGAGCG | GCGGTGTAGG  | AGTGCCCGTC  | GGGACGAACC  | 13560 |
| GCAACCGGAG  | CGTCCCCGTC  | TCGGTCGGGA | CCTCCGGGGT  | CGACCAGCTG  | CCGCCCGCGA  | 13620 |
| GCTCCGGAAT  | TAGCCGGCGT  | TGCACGTGTG | CCCGGGTCGA  | CCAGCAGGCG  | CCCGCGGGAC  | 13680 |
| GCAGCGGCGC  | ACGCACGCGA  | GGGCGTCGAT | TCCCTTTCGC  | GCGCCCGCGC  | CTCCACCGGC  | 13740 |
| CTCGGCCCGC  | GGTGGAGCTG  | GGACCACGCG | GAACCTCCCTC | TCCCACATTT  | TTTTTCAGCCC | 13800 |
| CACCGCGAGT  | TTGCGTCCGC  | GGGACCTTTA | AGAGGGAGTC  | ACTGCTGCCG  | TCAGCCAGTA  | 13860 |
| CTGCCTCCTC  | CTTTTTCGCT  | TTTAGGTTTT | GCTTGCCTTT  | TTTTTTTTTTT | TTTTTTTTTTT | 13920 |
| TTTTTCTTTT  | CTTTCTTTCT  | TTCTTTCTTT | CTTTCTTTCT  | TTCTTTCTTT  | CGCTTGCTTT  | 13980 |
| CTTCTTGTGT  | TCTCTTCTTG  | CTCTTCTCTC | GTCTGTCTCT  | CTCTCTCTCT  | CTCTCTCTGT  | 14040 |
| CTCTCGCTCT  | CGCCCTCTCT  | CTCTTCTCTC | TCTCTCTCTC  | TCTCTCTCTG  | TCTCTCGCTC  | 14100 |
| TCGCCCTCTC  | TCTCTCTCTT  | CTCTCTGTCT | CTCTCTCTCT  | CTCTCTCTCT  | CTCTCTCTCT  | 14160 |
| GTCTCTCTCG  | CCCTCTCTCT  | CTCTCTCTGT | CTCTCTCTGT  | GTCTCTCTCT  | TCCCTCCCT   | 14220 |
| CCCTCCCTCC  | CTCCCTCCCT  | CCCTCCCTTT | CCTTGGCGCC  | TTCTCGGCTC  | TTGAGACTTA  | 14280 |
| GCCGCTGTCT  | CGCCGTACCC  | CGGGTCGACC | GGCGGGCCTT  | CTCCACCGAG  | CGGCGTGCCA  | 14340 |
| CAGTGCCCGT  | CGGGACGAGC  | CGGACCCGCC | GCGTCCCCGT  | CTCGGTGCGC  | ACCTCCGGGG  | 14400 |
| TCGACCAGCT  | GCCGCCCCCG  | AGCTCCGGAC | TTAGCCGGCG  | TCTGCACGTG  | TCCCGGGTCG  | 14460 |
| ACCAGCAGGC  | GGCCGCGGGA  | CGCAGCGGCG | CACCGACGGA  | GGGCGCTGAT  | TCCCGTTTAC  | 14520 |
| GCGCCCGCGC  | CTCCACCGGC  | CTCGGCCCGC | CGTGGAGCTG  | GGACCACGCG  | GAACCTCCCTC | 14580 |
| TCCTACATTT  | TTTTTCAGCCC | CACCGCGAGT | TTGCGTCCGC  | GGGACCTTTA  | AGAGGGAGTC  | 14640 |
| ACTGCTGCCG  | TCAGCCAGTA  | CTGCCTCCTC | CTTTTTTCGCT | TTTAGGTTTT  | GCTTGCCCTTT | 14700 |
| TTTTTTTTTT  | TTTTTTTTTT  | TTTTTTCTTT | CTTTCTTTCT  | TTCTTTCTTT  | CTTTCTTTCT  | 14760 |
| TTCTTTCTTT  | CTTTCTCTCT  | CGTCTCTCTG | CTCTCTCTCT  | CGCTCGTTTC  | TTTCTTTCTC  | 14820 |
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| TTTCTCTCTC  | TCTCTGTCTC  | TCTCTCTCTC | TCTCTCTCTC  | TCTCTCTCTC  | CCTCCCTCCC  | 14940 |
| TCCCCCTCCC  | TCCCTCTCTC  | CCCTTCCTTG | GCGCCTTCTC  | GGCTCTTGAG  | ACTTAGCCGC  | 15000 |
| TGTCTCGCCG  | TGTCCCCGGT  | CGACCGGCGG | GCCTTCTCCA  | CCGAGCGGCG  | TGCCACAGTG  | 15060 |
| CCCGTCGGGA  | CGAGCCGGAC  | CCGCCGCGTC | CCCGTCTCGG  | TCGGCACCTC  | CGGGGTCGAC  | 15120 |

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| CAGGCGGCCG | CCGGACGCTG  | CGGCGCACCG | ACGCGAGGGC  | GTCGATTCCG  | GTTCACGCGC  | 15240 |
| CGGCGACCTC | CACCGGCCCTC | GGCCCCGGGT | GGAGCTGGGA  | CCACGCGGAA  | CTCCCTCTCC  | 15300 |
| CACATTTTTT | TCAGCCCCAC  | CGCGAGTTTG | CGTCCGCGGG  | ACTTTTAAGA  | GGGAGTCACT  | 15360 |
| GCTGCCGTCA | GCCAGTAATG  | CTTCCTCCTT | TTTTGCTTTT  | TGGTTTTGCC  | TTGCGTTTTTC | 15420 |
| TTTCTTTCTT | TCTTTCTTTC  | TTTCTTTCTT | TCTTTCTTTC  | TCTCTCTCTC  | TCTCTCTCTC  | 15480 |
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| TCCTTCCTTT | TTTCAATCTT  | ATTTTCTGAA | CGCTGCCGTG  | TATGAACATA  | CATCTACACA  | 15780 |
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| CAGCTTACGT | GGGCTGCGGT  | GCGGTGGGGT | GGGGTGGGGT  | GGGGTGGGGT  | GCAGAGAAAA  | 16200 |
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| TTATTTCTTT | CCTTCCTTCC  | TTCTTCCTTT | CCTTCCTTCC  | TTCTTCCTTT  | CCCTCCCTTA  | 16380 |
| CTGGCAGGGT | CTTCCTCTGT  | CTCTGCCGCG | CAGGATCACC  | CCAACCTCAA  | CGCTTTGGAC  | 16440 |
| CGACCAAACG | GTCTGTTCTG  | CTCTGATCCC | TCCCATCCCC  | ATTACCTGAG  | ACTACAGGCG  | 16500 |
| CGCACCACCA | CACCGGCTGA  | CTTTTATGTT | GTTTCTCATG  | TTTTCCGTAG  | GTAGGTATGT  | 16560 |
| GTGTGTGTGT | GTGTGTGTGT  | GTGTGTGTGT | GTGTGTGTGT  | GTGTGTGTGT  | GTGTGTATCT  | 16620 |
| ATGTATGTAC | GTATGTATGT  | ATGTATGTGA | GTGAGATGGG  | TTTCGGGGTT  | CTATCATGTT  | 16680 |
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| CTCTGAAAAA | TAGAACGATT  | AGCCGGGCCT | GGTGGCGTGG  | GCTTGGAATC  | ACGACCGCTC  | 18840 |
| GGGAGACTGG | GGCGGGCGAC  | TTGTTCCAAC | CGGGGAGGCC  | GAGGCCGCGA  | TGAGCTGAGA  | 18900 |
| TCGTGCCGTG | GCGATGCGGC  | CTGGATGACG | GAGCGAGACC  | CCGTCTCGAG  | AGAATCATGA  | 18960 |
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| TCTTCTGTCT  | TATTCTCTTT | CTCTCTCTGT  | CTCTCTCTCT | CTCTCCTTTA | CTGTCTGTTT | 25860 |
| CTCTCTCTCT  | CTCTCTCTTT | CTGCCTGTTT  | CTCTCTGTCT | GTCTCTGTCT | TTCTCTGTCT | 25920 |
| GTCTGCCTCT  | CTCTTTCTTT | TTCTGCCTCT  | CTCTGTCTCT | CTCTCTCTCT | CTCTGTCTCT | 25980 |
| ATCTTCTGTC  | TTACTCTGTT | TCCTTGCCTG  | CCTGCCTGTC | TGTGTGTCTG | TCTCTCTCTC | 26040 |
| TCTCTCTCTC  | TCTCTCTCCC | TCCCTTTCTC  | TTTCTCTGTC | TCTCTCTCTC | TTTCTGGGTG | 26100 |
| TTTCTCTCTG  | TCTCTCTGTC | CATCTCTGTC  | TTTCTATGTC | TGTCTCTCTC | TTTCTCTCTG | 26160 |
| TCTCTGTCTC  | TGCCCTCTCT | TCTCTCTCTC  | TCTCTCTCTC | TCTGTCTGTC | TCTCTCACTG | 26220 |
| TGTGTGTCTG  | TCTTCTGTCT | TACTCTCCTT  | CTCTGCCTGT | CCGTCTGTCT | GTCTGTCTCT | 26280 |
| CCCTCTCTCT  | CCCTCCCTTT | CTGTTTCTCT  | CTCTCTCTCT | TTCTGTCTGT | TTCTCTCTTT | 26340 |
| CTCTCTCTGT  | CTGTCTCTTT | CTCTGTCTGT  | CTGTCTCTCT | CTTTCTTTTT | CTCTGTCTCT | 26400 |
| CTGTCTCTCT  | CTGTGTCTGT | CTCTCTGTCT  | GTGCCTATCT | TCTGTCTTAC | TCTCTTTCTC | 26460 |
| TGGCTGTCTG  | CCTGTCTCTC | TCTCTCTCTC  | TGTCTGTCTC | CGTCCCTCTC | TCCCTCTCTG | 26520 |
| TCTGTTTCTC  | TCTCTGCCTC | TCTCTCTCTC  | TGTCTGTCTC | TTTCTCTGTC | TGTCTGTCTC | 26580 |
| TCTCTTTCTT  | TTTCTCTGTC | TCTCTGTCTC  | TCTCTGTGTC | TGTCTCTCTT | TCTGTGCCTA | 26640 |
| TCTTCTGTCT  | TACTCTCTTT | CTCTGGCTGT  | CTGCCTGTCT | CTCTCTCTCT | GCCTGTCTCC | 26700 |
| GTCCCTCCCT  | CCCTGTCTGT | CTGTTTCTCT  | CTCTGTCTCT | GTCTCTCTGT | CCATCTCTGT | 26760 |
| CTGTCTCTTT  | CTCTTTCTCT | CTCTCTGTCT  | CTGTCTCTCT | CTCTCTCTGC | CTGTCTCTCT | 26820 |



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|-------------|------------|------------|------------|-------------|-------------|-------|
| CACTGTGTCT  | GTCTTCTGTC | TTACTCTCTT | TCTCTTGCC  | GCCTCTCTGT  | CTGTCTGTCT  | 26880 |
| CTCTCCCTCC  | ATGTCTCTCT | CTCTCTCTCA | CTCACTCTCT | CTCCGTCTCT  | CTCTCTTTCT  | 26940 |
| GTCTGTTTCT  | CTCTCTGTCT | GTCTCTCTCC | CTCCATGTCT | CTCTCTCTCT  | CTCTCACTCA  | 27000 |
| CTCTCTCTCC  | GTCTCTCTCT | CTCTTTCTGT | CTGTTTCTCT | CTCTGTCTGT  | CTCTCTCCCT  | 27060 |
| CCATGTCTCT  | CTCTCTCCCT | CTCACTCACT | CTCTCTCCGT | CTCTCTCTCT  | CTTTCTGTCT  | 27120 |
| GTTTCTTTGT  | CTGTCTGTCT | GTCTGTCTGT | CTGTCTCTCT | CTCTCTCTCT  | CTCTCTCTCT  | 27180 |
| CTCTCTGTTT  | GTCTTTCTCC | CTCCCTGTCT | GTCTGTCTGT | CTCTCTCTCT  | CTGTCTCTGT  | 27240 |
| CTCTGTCTCT  | CTCTCTTTCT | CTTTCTGTCT | GTTTCTCTCT | ATCTCTCGCT  | GTCCATCTCT  | 27300 |
| GTCTTTCTAT  | GTCTGTCTCT | TTCTCTGTCA | GTCTGTCTGA | CACACCCGTG  | CCGGTAGGGC  | 27360 |
| CCTGCCCTTC  | CACGAGAGTG | AGAAGCGCGT | GCTTCGGTGC | TTAGAGAGGC  | CGAGAGGAAT  | 27420 |
| CTAGACAGGC  | GGGCCTTGCT | GGGCTTCCCC | ACTCGGTGTA | CGATTTCGGG  | AGGTCGAGGC  | 27480 |
| CGGGTCCCGG  | CTTGATGCG  | AGGGGCATT  | TCAGACTTTT | CTCTCGGTCA  | CGTGTGGCGT  | 27540 |
| CCGTACTTCT  | CCTATTTCCC | CGATAAGTCT | CCTCGACTTC | AACATAAACT  | GTTAAGGCCG  | 27600 |
| GACGCCAACA  | CGGCGAAACC | CCGTCTCTAC | TAAAAATACA | AAGCTGAGTC  | GGGAGCGGTG  | 27660 |
| GGGCAGGCC   | TGTAATGCCA | GCTCCTCGGG | AGGCTGAGGC | GGGAGAATCG  | CTTGAACCAG  | 27720 |
| GGAAGCGGAG  | GCTGCAGGGA | GCCGAGATCG | CGCCACTGCA | CTACGGCCCA  | GGCTGTAGAG  | 27780 |
| TGAGTGAGAC  | TCGGTCTCTA | AATAAATACG | GAAATTAATT | AATTCATTAA  | TTCTTTTCCC  | 27840 |
| TGCTGACGGA  | CATTTGCAGG | CAGGCATCGG | TTGTCTTCGG | GCATCACCTA  | GCGGCCACTG  | 27900 |
| TTATTGAAAG  | TCGACGTTGA | CACGGAGGGA | GGTCTCGCCG | ACTTCACCGA  | GCCTGGGGCA  | 27960 |
| ACGGGTTTCT  | CTCTCTCCCT | TCTGGAGGCC | CCTCCCTCTC | TCCCTCGTTG  | CCTAGGGAAC  | 28020 |
| CTCGCCTAGG  | GAACCTCCGC | CCTGGGGGCC | CTATTGTTCT | TTGATCGGCG  | CTTTACTTTT  | 28080 |
| CTTTGTGTTT  | TGGCGCCTAG | ACTCTTCTAC | TTGGGCTTTG | GGAAGGGTCA  | GTTTAATTTT  | 28140 |
| CAAGTTGCCC  | CCCGGCTCCC | CCCACTACCC | ACGTCCCTTC | ACCTTAATTT  | AGTGAGNCGG  | 28200 |
| TTAGGTGGGT  | TTCCCCCAAA | CCGCCCCCCC | CCCCCGCCT  | CCCAACACCC  | TGCTTGGA    | 28260 |
| CCTTCCAGAG  | CCACCCCGGT | GTGCCTCCGT | CTTCTCTCCC | CTTCCCCCAC  | CCCTTGCCGG  | 28320 |
| CGATCTCATT  | CTTGCCAGGC | TGACATTGTC | ATCGGTGGGC | GTCAGGCCCTC | ACTCGGGGGC  | 28380 |
| CACCGTTTTT  | GAAGATGGGG | GCGGCACGGT | CCCACTTCCC | CGGAGGCAGC  | TTGGGCCGAT  | 28440 |
| GGCATAGCCC  | CTTGACCCGC | GTGGGCAAGC | GGGCGGGTCT | GCAGTTGTGA  | GGCTTTTCCC  | 28500 |
| CCCGCTGCTT  | CCCGCTCAGG | CCTCCCTCCC | TAGGAAAGCT | TCACCTGGC   | TGGGTCTCGG  | 28560 |
| TCACCTTTTA  | TCACGATGTT | TTAGTTTCTC | CGCCCTCCGG | CCAGCAGAGT  | TTCACAATGC  | 28620 |
| GAAGGGCGCC  | ACGGCTCTAG | TCTGGGCCCT | CTCAGTACTT | GCCCAAAATA  | GAAACGCTTT  | 28680 |
| CTGAAAACCTA | ATAACTTTNC | TCACTTAAGA | TTTCCAGGGA | CGGCGCCTTG  | GCCCGTGT    | 28740 |
| GTGGCTTGT   | TTTGTTCGT  | TCTGTTTGT  | TTTGTTCGTG | TTTTTCCTTT  | CTCGTATGTC  | 28800 |
| TTTCTTTTCA  | GGTGAAGTAG | AAATCCCCAG | TTTTCAGGAA | GACGTCTATT  | TTCCCCAAGA  | 28860 |
| CACGTTAGCT  | GCCGTTTTTT | CCTGTTGTGA | ACTAGCGCTT | TTGTGACTCT  | CTCAACGCTG  | 28920 |
| CAGTGAGAGC  | CGGTTGATGT | TTACNATCCT | TCATCATGAC | ATCTTATTTT  | CTAGAAATCC  | 28980 |
| GTAGGCGAAT  | CCTGCTGCTG | CTCTGTTGTC | TGTTGTTGTT | GTTGTTGTTG  | TCGTCTGTTG  | 29040 |
| TGTTGTGCTT  | GTCGTTGTTG | TTGTCGTTGT | CGTTGTTTTT | AAAGTATACC  | CCGGCCACCG  | 29100 |
| TTTATGGGAT  | CAAAAGCATT | ATAAAATATG | TGTGATTATT | TCTTGAGCAC  | GCCCTTCCCTC | 29160 |
| CCCTCTCTCT  | TGTCTCTCTG | TCTGTCTCTG | TCTCTCTCTT | TCTCTGTCTG  | TCTTCTCTCT  | 29220 |
| CTCTCTCTCT  | CTGTGCTCTG | CTCTCTCTCT | CTCTCTGTTT | CTCTCTCTCT  | GCCTCTCTCT  | 29280 |
| CTCTCTCTCT  | CTCTGCCTGT | CTCTCTCACT | GTGTCTGTCT | TCTGTCTTAC  | TCCCTTTCTC  | 29340 |
| TGTCTGTCTG  | TCGGTCTCTC | TCTCTCTCTC | TCCCTGTCTG | TATGTTTCTC  | TCTGTCTCTG  | 29400 |
| TCTCTCTCTC  | TCTTTCTGTT | TCTCTCTCTC | CGTCTCTGTC | TTTCTCTGAC  | TGTCTCTCTC  | 29460 |
| TTTCTTTCTC  | TCTGTCTCTC | TCTGCCTGTC | TCTCTCACTC | TGTCTTCTGT  | CTTATCTCTC  | 29520 |
| TCTCTGCCTG  | CTGTGCTCTC | TCATCTCTCT | TCTCTGTGTG | TCTTCTCTCT  | TCTTCTGTT   | 29580 |
| TCTCTCTGTC  | TCTCTGTCCG | TCTCTGTCTT | TCTCTGTCTG | TCTCTTTGTC  | TGTCTGTCTT  | 29640 |
| TGTCTTTCTT  | TCTCTCTGTC | TCTGTCTCTC | TCAGTGTGTC | TGTCTTCTGT  | CTTAGTCTCT  | 29700 |
| CTCTCTCTCT  | CTCCCTGTCT | GTCTGTCTCT | CTCTCTCTCT | CCCCCTGTCT  | GTTTCTCTCT  | 29760 |
| CTCTCTCTCT  | CTCTCTCTCT | CTCTGTCTTT | GTCTTTCTTT | CTGTCTCTGT  | CTCTCTCTCT  | 29820 |
| CTCTCTGTGT  | CTCTGTCTTC | TGCTTTACTG | TCTTTCTCTG | CCTGTCTGTC  | TGCTGTCTCT  | 29880 |
| TCTCTGTCTG  | TCTCTCTCTC | TCTCTCCCCC | TGTCGGCTGT | TTCTCTGTCT  | CTGTCTGTGT  | 29940 |
| CTCTCTTTCT  | GTCTGTTTCT | CTCTGTCTGT | CTTTCTCTCT | CTGTCTCTTT  | CTCTCTGTCT  | 30000 |
| CTCTGTCTGT  | CTCTGTCTCT | CTCTGTCTCT | CTCTCTCTCT | GTGGGGGTGT  | GTGTGTGTGT  | 30060 |
| GTGTATGTGT  | GCTGTGTGTG | GTGTGTGTGT | TGCTCTCTCT | TCTTACTCTC  | TTTCTCTGCC  | 30120 |
| TGTCTGTCTG  | CTGTGTCTGT | TGTCTCTCTC | TCTCTGCCTG | TCTCTCTCCC  | TTCCGTGTCTG | 30180 |
| TTTCTCTCTC  | TTTCTGTTTC | TCTCTGTCTC | TGTCCATCTC | TGTCTTTCTC  | CGTCTGTCTC  | 30240 |
| TTTATCTGTC  | TCTCTCCGTC | TGTCTCTTTA | TCTGTCTCTC | TCTCTCTTTT  | TGTCTTTCTC  | 30300 |
| TCTCTGTGTA  | TCGTTGTCTC | TCTCTGTCTG | TCTCTGTCTC | TGTCTCTCTG  | TCTCTCTCTC  | 30360 |
| TCTCTGTCTC  | TCTCTGTCTC | TCTGTCCGTC | TGTCTGTCTC | GGTCTCTGCG  | TCTCGTATC   | 30420 |
| TCCCGCCCTC  | TCTTTTGTG  | CAAAAGAAGC | TCAAGTACAT | CTAATCTAAT  | CCCTTACCAA  | 30480 |
| GGCCTGAATT  | CTTCACTTCT | GACATCCCAG | ATTTGATCTC | CCTACAGAAT  | GCTGTACAGA  | 30540 |
| ACTGGCGAGT  | TGATTTCTGG | ACTTGGATAC | CTCATAGAAA | CTACATATGA  | ATAAAGATCC  | 30600 |
| AATCCTAAAA  | TCTGGGGTGG | CTTCTCCCTC | GACTGTCTCG | AAAAATCGTA  | CCTCTGTTCC  | 30660 |
| CCTAGGATGC  | CGGAAGAGTT | TTCTCAATGT | GCATCTGCCC | GTGTCTTAAG  | TGATCTGTGA  | 30720 |

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|-------------|-------------|-------------|-------------|-------------|-------------|-------|
| CCGAGCCCTG  | TCCGTCCTGT  | CTCAAATATG  | TACGTGCAAA  | CACTTCTCTC  | CATTTCCACA  | 30780 |
| ACTACCCACG  | GCCCCCTTGT  | GAACCACTGG  | CTCTTTGAAA  | AAAAATCCCAG | AAGTGGTFFF  | 30840 |
| GGCTTTTTTG  | CTAGGAGGCC  | TAAGCCTGCT  | GAGAACTTTC  | CTGCCCAGGA  | TCCTCGGGAC  | 30900 |
| CATGCTTGCT  | AGCGCTGGAT  | GAGTCTCTGG  | AAGGACGCAC  | GGGACTCCGC  | AAAGCTGACC  | 30960 |
| TGTCCCAACG  | AGGTCAAATG  | GATACCTCTG  | CATTGGCCCCG | AGGCCTCCGA  | AGTACATCAC  | 31020 |
| CGTCACCAAC  | CGTCACCGTC  | AGCATCCTTG  | TGAGCCTGCC  | CAAGGCCCCCG | CCTCCGGGGA  | 31080 |
| GACTCTTGGG  | AGCCCCGGCCT | TCGTCCGGCTA | AAGTCCAAAG  | GGATGGTGAC  | TTCCACCCAC  | 31140 |
| AAGGTCCAC   | TGAACGGCGA  | AGATGTGGAG  | CGTAGGTCAG  | AGAGGGGACC  | AGGAGGGGAG  | 31200 |
| ACGTCCCGAC  | AGGCGACGAG  | TTCCCAAGGC  | TCTGGCCACC  | CCACCCACGC  | CCCACGCCCC  | 31260 |
| ACGTCCCGGG  | CACCCGCGGG  | ACACCGCCGC  | TTTATCCCCCT | CCTCTGTCCA  | CAGCCGGCCC  | 31320 |
| CACCCACCA   | CGCAACCCAC  | GCACACACGC  | TGGAGGTTCC  | AAAACCACAC  | GGTGTGACTA  | 31380 |
| GAGCCTGACG  | GAGCGAGAGC  | CCATTTCACG  | AGGTGGGAGG  | GGTGGGGGTG  | GGGTGGGTTG  | 31440 |
| GGGGTTGTGG  | GGTCTGTGGC  | GAGCCCAGATT | CTCCCTCTTG  | GGTGGCTACA  | GGCTAGAAAT  | 31500 |
| GAATATCGCT  | TCTTGGGGGG  | AGGGGCTTCC  | TTAGGCCATC  | ACCGCTTGCG  | GGACTACCTC  | 31560 |
| TCAAACCCTC  | CCTTGAGGCC  | ACAAAATAGA  | TTCCACCCCA  | CCCATCGACG  | TTTCCCCCGG  | 31620 |
| GTGCTGGATG  | TATCCTGTCA  | AGAGACCTGA  | GCCTGACACC  | GTCGAATTAA  | ACACCTTGAC  | 31680 |
| TGGCTTTTGT  | TGTTTGTGTT  | TTTCTGAGAT  | GGAGTCTTGC  | TCTGTCCCCC  | AGGCTGGAGT  | 31740 |
| GCAGTGGCGT  | GATCTCAGCT  | CAC TGGAAAC | TCTGCCTCCT  | GGGTTCAGT   | GATTCTCCTG  | 31800 |
| TCTCAGCGCC  | ACCATGGCCG  | GCTCATTTTT  | TTTTTTTTTTT | TTTTTTGGTAG | ACACGGGGTT  | 31860 |
| TCACCCTCTT  | TCATTGGTTT  | TCACTGGAGA  | TTCTAGATTG  | GAGCCACACC  | TCATTCCGTG  | 31920 |
| CCACGAGAG   | ACTTCTTTTT  | TTTTTTTTTTT | TTTTTAAGCG  | CAACGCAACA  | TGTCTGCCTT  | 31980 |
| ATTTGAGTGG  | CTTCTATAT   | CATTATAATT  | GTGTTATAGA  | TGAAGAAACG  | GTATTAACA   | 32040 |
| CTGTGTGAAT  | GTGAAGGAAA  | GTGAAGGAAA  | AAGAAAGGCT  | ATCTATTTTG  | TGGTTAGAAT  | 32100 |
| AAAGTTGCTC  | AGTATTTAGA  | AGCTACCTAA  | ATACGTCAGC  | ATTTACACTC  | TTCCTAGTAA  | 32160 |
| AAGCTGGCCG  | ATCTGAATAA  | TCCTCCTTTA  | AACAAACACA  | ATTTTGTGATA | GGGTTAAGAT  | 32220 |
| TTTTTTAAGA  | ATGCGACTCC  | TGCAAAATAG  | CTGAACAGAC  | GATACACATT  | TAAAAAATA   | 32280 |
| ACAACACAAG  | GATCAACCAG  | ACTTGGGAAA  | AAATCGAAAA  | CCACACAAGT  | CTTATGAAGA  | 32340 |
| ACTGAGTTCT  | TAAAATAGGA  | CGGAGAACGT  | AGCTATCGGA  | AGAGAAGGCA  | GTATTGGCAA  | 32400 |
| GTTGATTGTT  | ACGTTGGTCA  | GCAGTAGCTG  | GCATATCTTT  | TTTGGCCATC  | TTTCGGGCAA  | 32460 |
| TGTAACACT   | ACAGCAAAAT  | GAGATATGAT  | CCATTAAACA  | ACATATTCGC  | AAATCAAAAA  | 32520 |
| GTGTTTCAGT  | AATATAATGC  | TTTCAATTTA  | GAAGCAAATC  | AAATGATAGA  | ACTCCACTGC  | 32580 |
| TGTAATAAGT  | CACCCCAAG   | ATCACCGTAT  | CTGACAAAAAT | AACTACCACA  | GGGTTATGAC  | 32640 |
| TTCAGAATCA  | TACTTTCTTC  | TTGATATTTA  | CTTATGTATT  | TATTTTFTTT  | AATTTATTTT  | 32700 |
| TCTTGAGACG  | CGTCTCGCTC  | TGTCGCCCCAG | GCTGGAGTGC  | GATGGTGTGA  | TCTCGGCTCA  | 32760 |
| CTGCAACCGC  | CACCTCCCTG  | GGTTCAGCGC  | ATTCTCTCTG  | CTCAGCCTCC  | CGAGTAGCTG  | 32820 |
| GGACTACAGG  | TGCCCGCCAC  | CACGCGCCAG  | TAATCTTTAT  | ACTTTTAATA  | GAGACGGGGT  | 32880 |
| TTCACCGTGT  | CGGCCCCGAT  | GGTCTCGATC  | CTTTGACCTC  | GTGACCCGCC  | CGCCTCGGCC  | 32940 |
| TCCCAAAGTG  | CTGGGATGAC  | AGGCGTGAGC  | CACTGAGCCC  | GGCCTTCTCT  | TGACGTTTAA  | 33000 |
| ACTATGAAGT  | CAGTCCAGAG  | AAACGCAATA  | AATGTCAACG  | GTGAGGATGG  | TGTTGAGGCA  | 33060 |
| GAAGTAGGAC  | CACACTTTTT  | CCTATCTTAT  | TCAGTTGATA  | ACAATATGAC  | CTAGGTAGTA  | 33120 |
| ATTTCTATAG  | TGCCTACTTA  | TACACGAGTA  | TACAAAGAGTA | AAACAGAGAG  | ACTGCTAAAT  | 33180 |
| TAAAGGGTAC  | GTGAAGTTCT  | TCATAGTAAC  | TCCGTAAACT  | GGAACACTGT  | CAAAAAGCAG  | 33240 |
| CAGCTAGTGA  | ATTGTTTCCA  | TGTATTTTTT  | TATTATCCAA  | TAAGTGAAC   | ATGCTATTCC  | 33300 |
| TTTCCAGTCT  | CCCAAGCACT  | TCTTGTCCCC  | ATCACCACCT  | CGGTGCTCGA  | AGAAAAAGTA  | 33360 |
| AGCAAAATCA  | GGACACACA   | CTAAAGAAAC  | ACACACACAA  | ACCAAAGACA  | ACTACAGCGT  | 33420 |
| CTGCAAAAGT  | TTGCTAGAAG  | ACTGAAACTG  | TTGAGTATAA  | GGATCTGGTA  | TTCTACGATC  | 33480 |
| ATGAGTTCAC  | TTCAGAGTTT  | GTTCAAGACA  | TACGTTTCGT  | AAGGAAACAT  | CTTAGTTAGA  | 33540 |
| AGTTATTTCAG | CAGTAGGTAC  | CATCCCTAAG  | TATTTTTTCAC | CAAATCCGTG  | ACAATAAAGA  | 33600 |
| GCTATCTAAC  | CAGAAAAAT   | AGCGAGTACG  | GGCACCATCC  | ATAGGGCTTT  | GTCTTTACGC  | 33660 |
| TTCATTAGCA  | CTTACCATGC  | CTTACAATGT  | CTAGGATTGA  | CCCTGATAGC  | ATTTGCAAAA  | 33720 |
| CAAGCTAATG  | CTTTGTCCAG  | TTCTTCAGTG  | AAGACAACCT  | ACGCCCTAAT  | GCGCTATAGG  | 33780 |
| CATAAGCATC  | ATTTGGATCC  | ACTTCGAGAG  | TTCTCTGGAA  | GAATTGAATC  | GCAATATCGT  | 33840 |
| GTTCCCGTTT  | GCAGACCGAA  | ACAGTTTCCC  | TGCAGCACAC  | CAGGCCTCTG  | GCTGGCGAAT  | 33900 |
| TTTTATCCAT  | GTCTGTGAAG  | TCTTTGGACA  | GAAC TGAAG  | AGCAACCTCT  | TTCCGGAGGAT | 33960 |
| GCCAAAGTGT  | TGTAGAGTAG  | ATCTCCATGC  | CTTCGACTCT  | GTAATTCTCA  | ATCCTCCTAA  | 34020 |
| CCTCTGAGAA  | TTGTCTTTCA  | GCTTGCGTGG  | ACTCTGAAAG  | TTTACAATAG  | GCCNTTTCCG  | 34080 |
| ATTTGGCACA  | GTACCCAACC  | GGTATTGCAG  | TGGTGAGAAG  | CTAGATGGCT  | CAAGATGCTG  | 34140 |
| ATAGCTTCTT  | TGCCGTGGTA  | AGAACACAAA  | GCTAAATAAC  | CTTTCCCCCT  | TTCACGAAGA  | 34200 |
| AGGCTCATCA  | AGCCTTCCGC  | TGCTGCTTTT  | TGTAGATTAA  | AAGCCTGAAT  | CTGAGGCGCG  | 34260 |
| ATTGCGGCTA  | TTTTCCCTTC  | TGAAATGACG  | GAAGAGTCCA  | ATTTTGTGTC  | TTCCAGGCTA  | 34320 |
| TCACTTATGT  | TCGGTGAGGT  | TATTGCTCCT  | TTATTAGTTT  | TACTTTTGGT  | TCTTCTGTTT  | 34380 |
| GGGATTTTAG  | GTGGAACCTT  | CATTTTAAAT  | TTTCTCCTAA  | TTCTCCTCGG  | TTGTGGAGCT  | 34440 |
| GTCAC TAGTC | AAGAGTCGTG  | AATTTCTTCG  | AGGNCGGTGC  | ATTTGGGGGA  | GATGCCATAG  | 34500 |
| TGGGGCTCAA  | TACCTGAGGT  | GTTGCCCTTG  | TCGGCGGACC  | AGAACTTTGT  | GTTTTTGCAA  | 34560 |
| GGACTGGAGT  | TACCTTTCGG  | CTCTTTCCTC  | TCTGCGAGAA  | GACAGACGGT  | GTTCCGGTTT  | 34620 |



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|-------------|------------|-------------|------------|-------------|-------------|-------|
| GGCCGATTCT  | GGCAACAGGC | TTTTCTGAAG  | GGGCTCCGGT | GGATGGCAGC  | TCAGTGACAG  | 34680 |
| ACGGTGTCTC  | ATACCAGTGC | AGTTTTGTCA  | ATAGGGTCCG | TCTCCGGGAC  | TTGGGGTTTC  | 34740 |
| TAATGGCAAA  | ATGCCAACAC | TTGGGGTTAA  | TGGACTAACA | GCTGCTGGTC  | CTCCTAATAA  | 34800 |
| ACTTCGACCA  | GTTTTTGGTT | TATGTTGAAC  | CTGTTTAGAT | CATATGGAAAG | TTCCTGTTCC  | 34860 |
| CAGTGGGACA  | GTATCAGGTG | AAAGGACAGC  | TGAATCGATA | GAAGACACTG  | GGGAGTCTGT  | 34920 |
| ATTC AAGGAG | TACTTTGAAT | TGGAAGATTG  | TAAATTCCAT | CCGTTTCATT  | CGACGGTGTC  | 34980 |
| CTGGGGTGTT  | TCCGTAAGAA | CGGTCTCGGG  | CTGTCTGTGA | CATAAACTAG  | GACGAGGTCC  | 35040 |
| AAGTGTGTG   | GCGCAACACT | TGGACAGGCA  | GTTGCTAAAG | CTCTCTAGAG  | AGGTGAATCA  | 35100 |
| AAATGTTTGG  | TCAGGATCTG | GCTTTTCCCC  | CCTATTTTAC | ATCATGATTG  | AAAGGGACAC  | 35160 |
| CAGAGGAAAG  | GATTTCAACG | AAGGCTCTTT  | TGGTCACATT | CTGATCCTTT  | GGTAAGCCGA  | 35220 |
| TCTGTCTTGC  | AATATACATG | TCCCCGACGAT | GGAAGGGGAA | AGCGAGCTGA  | ATCACC AAAC | 35280 |
| TCAGGAACGA  | TAATATCATC | GTGGCTTTTC  | TGCTTATGAA | ACACTCCACC  | CGATAAGATT  | 35340 |
| TGATCCCCCT  | CTGCAAGCTT | GCTGAGATCA  | ACACAACATT | TCGCAAGCAG  | GCATTTGCAT  | 35400 |
| TGCGGGGTAG  | TACAACTGTG | TCCTTTCAAG  | AGTCTATATG | TTTTATAGGC  | CTTTCCTGAG  | 35460 |
| CGGTAAGAAC  | AGGTCGCCAG | TAAGAACAAG  | GCTTCTTCTG | AGTGTACTTC  | TGCATAAAGG  | 35520 |
| CGTTCTGCGG  | GGGAAACCGC | ATCTCGGTAG  | GCATAGTGGT | TTAGTGCTTG  | CCATATAGCA  | 35580 |
| GCCTGGACGG  | GTCCCTGCAG | CACCGCCATC  | CTCGAGGCTC | AGGCCCACTT  | TCTGCAGTGC  | 35640 |
| CACAGGCACC  | CCCCCCCCCC | CATAGCGGCT  | CCGGCCCCGG | CAGCCCCGGC  | TCATTTAAAG  | 35700 |
| GCACCAGCCG  | CCGTTACCGG | GGGATGGGGG  | AGTCCGAGAC | AGAATGACTT  | CTTTATCCTG  | 35760 |
| CTGACTCTGG  | AAAGCCCCGG | GCCTTGTGAT  | CCATTGCAAA | CCGAGAGTCA  | CCTCGTGTTC  | 35820 |
| AGAACACGGA  | TCCACTCCCA | AGTTCAGTGG  | GGGGATGTGA | GGGGTGTGGC  | AGGTAGGACG  | 35880 |
| AAGGACTCTC  | TTCTTCTGTA | TTGCGTCTGG  | ACGAGTGGGC | CTAGGGCTGG  | AGCTCTCTCC  | 35940 |
| GTGCGGACCG  | CTGACTCCCT | CTACCTTGGG  | TTCCCTCGGC | CCCACCTTGG  | AACGCCGGGC  | 36000 |
| CTTGGCAGAT  | TCTGGCCCTT | TCTGGCCCTT  | CAGTCGCTGT | CAGAAACCCC  | ATCTCATGCT  | 36060 |
| CGGATGCCCC  | GAGTGACTGT | GGCTCGCACC  | TCTCCGGAAA | CATTGGAAAT  | CTCTCCTCTA  | 36120 |
| CGCGCGGCCA  | CCTGAAACCA | CAGGAGCTCG  | GGACACACGT | GCTTTCGGGA  | GAGAATGCTG  | 36180 |
| AGAGTCTCTC  | GCCGACTCTC | TCTTGACTTG  | AGTTCTTCGT | GGGTGCGTGG  | TTAAGACGTA  | 36240 |
| GTGAGACCAG  | ATGTATTAAC | TCAGGCCGGG  | TGCTGGTGGC | TCACGCCTGT  | AACCCCAACA  | 36300 |
| CTTTGGGAGG  | CCGAGGCCGT | AGGATCCCTC  | GAGGAATCGC | CTAACCTTGG  | GGAGGTTGAG  | 36360 |
| GTTGCAGTGA  | GTGAGCCATA | GTTGTGTGAC  | TGTGCTCCAG | TCTGGGCGAA  | AGACAGAATG  | 36420 |
| AGGCCCTGCC  | ACAGGCAGGC | AGGCAGGCAG  | GCAGGCAGAA | AGACAACAGC  | TGTATTATGT  | 36480 |
| TCTTCTCAGG  | GTAGGAAGCA | AAAATAACAG  | AATACAGCAC | TTAATTAATT  | TTTTTTTTTT  | 36540 |
| CCTTCGGACG  | GAGTTTCACT | CTTGGTGCCC  | ACGCTGGAGT | GCAGTGGCAC  | CATCTCGGCT  | 36600 |
| CACCGCAACC  | TCCACCTCCC | GCGTTCAAGC  | GATTCTCCTG | CCTCAGCCTC  | CTGAGTAGCT  | 36660 |
| GGGATTACAG  | GGAGGAGCCA | CCACACCCAG  | CTGATTTTGT | ATTGTTAGTA  | GAGACGGCAT  | 36720 |
| TCTCTCATGT  | GGGTACGGCT | GGTCTCGAAC  | TGGCATCCCC | AGTGGATCTG  | CCCGCCCCGG  | 36780 |
| CCTCCCAAAG  | TGCTGGGGTG | ACAGGCGTGA  | GCCATCGTGA | CTGGCCGGCT  | ACGTTTATTT  | 36840 |
| ATTTATTTTT  | TTAATTATTT | TACTTTTTTT  | TAGTTTTCCA | TTTTAATCTA  | TTTATTTATT  | 36900 |
| TACATTTATT  | TATTTATTTA | TTTATTTACT  | TATTTATTTA | TTTTCGAGAC  | AGACTCTCGC  | 36960 |
| TCTGCTGCCC  | AGGCTGGAGT | GCAGCGGCGT  | GATCTCGGCT | CACTGCAACG  | TCCGCCTCCC  | 37020 |
| GGGTTACAGC  | CATTCTCCTG | CCTCAGCCTC  | CCAAGTAGCT | GGGACTACAG  | GCGCCCGCCA  | 37080 |
| CCGTGCCCGG  | CTAACTTTTT | GTATTTTGAG  | TAGAGATGGG | GTTTCACTGT  | GGTAGCCAGG  | 37140 |
| ATGGTCTCGA  | TCTCCTGACC | CCGTGATCCG  | TCCACCTCGG | CCTCCCAAAG  | TGCTGGGATG  | 37200 |
| ACAGGCGTGA  | GCCACCGGCC | CCGGCCTATT  | TATCTATTTA | TTAACTTTGA  | GTCCAGGTTA  | 37260 |
| TGAAACAGT   | TAGTTTTTGT | AATTTTTTTT  | TTTTTTTTTT | TTTTTTGAGA  | CGAGGTTTCA  | 37320 |
| CCGTGTTGCC  | AAGGCTTGGT | CCGAGGGATC  | CACCGGCCCT | CGGCCTCCCA  | AAAGTGCGGG  | 37380 |
| GATGACAGGC  | GCGAGCCTAC | CGCGCCCGGA  | CCCCCCTTTT | CCCCCTCCCC  | CGCTTGCTCT  | 37440 |
| CCCGACAGAC  | AGTTTCACGG | CAGAGCGTTT  | GGCTGGCGTG | CTTAAACTCA  | TTCTAAATAG  | 37500 |
| AAATTTGGGA  | CGTCAGCTTC | TGGCCTCACG  | GACTCTGAGC | CGAGGAGTCC  | CCTGGTCTGT  | 37560 |
| CTATCACAGG  | ACCGTACACG | TAAGGAGGAG  | AAAAATCGTA | ACGTTCAAAG  | TCAGTCATTT  | 37620 |
| TGTGATACAG  | AAATACACGG | ATTCACCCAA  | AACACAGAAA | CCAGTCTTTT  | AGAAATGGCC  | 37680 |
| TTAGCCCTGG  | TGTCCGTGCC | AGTGATTCTT  | TTGCGTTTGG | ACCTTGACTG  | AGAGGATTCC  | 37740 |
| CAGTCGGTCT  | CTCGTCTCTG | GACGGAAGTT  | CCAGATGATC | CGATGGGTGG  | GGGACTTAGG  | 37800 |
| CTGCGTCCCC  | CCAGGAGCCC | TGGTCGATTA  | GTTGTGGGGA | TCGCCTTGGA  | GGGCGCGGTG  | 37860 |
| ACCCACTGTG  | CTGTGGGAGC | CTCCATCCTT  | CCCCCACCCT | CCTCCCCAGG  | GGGATCCCAA  | 37920 |
| TTCAATCCGG  | GCTGACACGC | TCACTGGCAG  | GCGTCGGGCA | TCACCTAGCG  | GTCACTGTTA  | 37980 |
| CTCTGAAAAC  | GGAGGCCTCA | CAGAGGAAGG  | GAGCACCAGG | CCGCCTGCGC  | ACAGCCTGGG  | 38040 |
| GCAACTGTGT  | CTTCTCCACC | GCCCCCGCCC  | CCACCTCCAA | GTTCTCTCCT  | CCCTTGTTGC  | 38100 |
| CTAGGAAATC  | GCCACTTTGA | CGACCGGGTC  | TGATTGACCT | TTGATCAGGC  | AAAAACGAAC  | 38160 |
| AAACAGATAA  | ATAAATAAAA | TAACACAAAA  | GTAACTAACT | AAATAAAAAA  | AGTCAATACA  | 38220 |
| ACCCATTACA  | ATACAATAAG | ATACGATACG  | ATAGGATGCG | ATAGGATACG  | ATAGGATACA  | 38280 |
| ATACAATAGG  | ATACGATACA | ATACAATACA  | ATACAATACA | ATACAATACA  | ATACAATACA  | 38340 |
| ATACAATACA  | ATACAATACG | CCGGGCGCGG  | TGGCTCATGC | CTGTCATCCC  | GTCACCTTGG  | 38400 |
| GATGCCGAGG  | TGGACGCATC | ACCTGAAGTC  | GGGAGTTGGA | GACAAAGCCG  | ACCAACATGG  | 38460 |
| AGAAATCCCG  | TCTCAATTGA | AAATACAAAA  | CTAGCCGGGC | GCGGTGGCAC  | ATGCCTATAA  | 38520 |

TCCCAGCTGC TAGGAAGGCT GAGGCAGGAG AATCGCTTGA ACCTGGGAAG CGGAGGTTGC 38580  
 AGTGAGCCGA GATTGCGCCA TCGCACTCCA GTCTGAGCAA CAAGAGCGAA ACTCCGTCTC 38640  
 AAAAAATAAA ACATAAATAA ATACATACAT ACATACATAC ATACATACAT ACATACATAC 38700  
 ATAAATTAAA ATAAATAAAT AAAATAAAAT AAATAAATGG GCCCTGCGCG GTGGCTCAAG 38760  
 CCTGTCTATCC CCTCACTTTG GGAGGCCAAG GCCGGTGGAT CAAGAGGCGG TCAGACCAAC 38820  
 AGGGCCAGTA TGGTGAAACC CCGTCTCTAC TCACAATACA CAACATTAGC CGGGCGCTGT 38880  
 GCTGTGCTGT ACTGTCTGTA ATCCCAGCTA CTCGGGAGGC CGAGCTGAGG CAGGAGAATC 38940  
 GCTTGAACCT GGGAGGCGGA GGTGTCAGTG AGCCGAGATC GCGCCACTGC AACCAGCCT 39000  
 GGGCGACAGA GCGAGACTCC GTCTCCAAAA AATGAAAATG AAAATGAAAC GCAACAAAAT 39060  
 AATTAAAAAG TGAGTTTCTG GGGAAAAAGA AGAAAAGAAA AAAGAAAAAA ACAACAAAAC 39120  
 AGAACAACCC CACCGTGACA TACACGTACG CTTCTCGCCT TTCGAGGCCT CAAACACGTT 39180  
 AGGAATTATG CGTGATTCTT TTTTTTAACT TCATTTTATG TTATTATCAT GATTGATGTT 39240  
 TCGAGACGGA GTCTCGGAGG CCCGCCCTCC CTGGTTGCCC AGACAACCCC GGGAGACAGA 39300  
 CCCTGGCTGG GCCCGATTGT TCTTCTCCTT GGTCAGGGGT TTCCTTGTCT TTCTTCGTGT 39360  
 CTTTAACCCG CGTGGAATCT TCCGCCTCGG GTTTGACAGA TGGCAGCTCC ACTTTAGGCC 39420  
 TTGTTGTTGT TGGGGACTTT CCTGATTCTC CCCAGATGTA GTGAAAGCAG GTAGATTGCC 39480  
 TTGCCTGGCC TTGCCTGGCC TTGCCTTTTT TTTCTTTCTT TCTTTCTTTA TTACTTTCTC 39540  
 TTTTCTTCTT TCTTCTTCTT CTTTTTTTTG AGACAGAGTT TCACTCTTGT TGCCAGGCT 39600  
 AGAGGGCAAT GGCGCGATCT CGGCTCACCG CACCCTCCGC CTCCAGGTT CAAGCGATTC 39660  
 TCCTGCCTCA GCCTCCTGAT TAGCTGGGAT TACAGGCATG GGCCACCGTG CTGGCTGATG 39720  
 TTTGTACTTT TAGTAGAGAC GGTGTTTTTC CATGTTGGTC AGGCTGGTCT CCCACTCCCA 39780  
 ACCTCAGGTG GTCCGCCTGC CTAGCCTCC CAAAGTGCTG GGATGACAGG CGTGCAACCG 39840  
 CGCCAGCCTT CTCTCTCTCT CTCTCTCTCT CTCGCTCGCT TGCTTGCTTG CTTTCGTGCT 39900  
 TTCTTGCTTT CCCGTTTTCT TGCTTTCTTT CTTTCTTTCT TTTCTTTCTT GCTTGCTTTT 39960  
 TTGCTTGCTT GCTTGCTTTT GTGCTTTCTT GCTTTCTCTG TTTCTTTCTT TCTTTCTTTT 40020  
 TTTCTTTCTT TTGTTTCTTT CTGCTTGCTT TTCTTGCTTG CTTGCTTGCT TTCGTGCTTT 40080  
 CTTGCTTTCC TGTTTTCTTT CTTTTCTTCT TCTTTTCTT TCTTTCTTGC TTGCTTTCTT 40140  
 GCTTGCTTGC TTTCGTGCTT TCTTGTTTTT TCGATTTCTT TCTTTCTTTT GTTTCCTTCC 40200  
 TGCTTGCTTT CTTGCTTGCT TGCTTTCTGT CTTCTTGCTT TCCTGTTTTT TTTCTTTCTT 40260  
 TCTTTCTTTT GTTTCTTTCT TGCTTGCTTT CTTGCTTGCT TGCTTTCTGT CTGTCTTGTT 40320  
 TCTCGATTTT TTTCTTTCTT TTGTTTCTTT CCTGCTTGCT TTCTTGCTTG ATTGCTTTCT 40380  
 TGCTTTCTTG CTTTCTTGTT TTTTCTTTT CTTTCTTTT GTTCTTTCTT GCTTCTTGTT 40440  
 TTTCTTGCTT TCTTGCTTGC TTGCTTTCTG GCTTTCTTGT TTTCTTGCTT TCTTTCTTTT 40500  
 GTTTCTTTCT TGCTTGCTTT CTGCTTTCTT TGTTTTCTTG CTTTCTTGCT TGCTTGCTTT 40560  
 CGTGCTTTCT TTCTTGCTTT CTTTCTTTT TTTCTTTTCT TTTTCTTTCT TTCTTGCTTT 40620  
 CTTTCTTTT ATCATATCT TTCTTTCTTT CTTTCTTTT TTTCTTTCTT TCTATCTTCT 40680  
 TTTCTTTCTT CTTTCTTTT TAGAGTGCAA TGGCGCGATC TTGGCTCACC GCACCTTCCG 40740  
 TTCACTCTTG TTTCCACGGC TAGAGTGCAA TGGCGCGATC TTGGCTCACC GCACCTTCCG 40800  
 CCTCCCGGGT TCGAGCGCTT CTCCTGCCTC CAGCCTCCCG ATTAGCGGGG ATTGACAGGG 40860  
 AGGCACCCCC ACGCCTGGCT TGGCTGATGT TTGTGTTTTT AGTAGGCACG CCGTGTCTCT 40920  
 CCATGTTGCT CAGGCTGGT TCCAACTCCC GACCTCCTGT GATCGCGCCA CCTCGCTTCT 40980  
 TCGAAGTGCT GGGATGACGG GCGTGACGAC CGTGCCCGGC CTGTTGACTC ATTTGCTTTT 41040  
 TTTATTTCTT TCGTTTCCAC GCGTTTACTT ATATGTATTA ATGTAAACGT TTCTGTACGC 41100  
 TTATATGCAA ACAACGACAA CGTGATATCT TGCATTGAAT ACTCTTGCGT ATGGTAAATA 41160  
 CGTATCGGTT GTATGGAAAT AGACTTCTGT ATGATAGATG TAGGTGTCTG TGTATACAA 41220  
 ATAAATACAC ATCGCTCTAT AAAGAAGGGA TCGTCGATAA AGACGTTTAT TTTACGTATG 41280  
 AAAAGCGTCG TATTTATGTG TGTAATGAA CCGAGCGTAC GTAGTTATCT CTGTTTTCTT 41340  
 TCTTCTCTCT CTTCTGTGTT TTCTTCTTCT CTTTCTTCTT TTCTCTCTCT CTTTAGGTTT 41400  
 TTCTTCTCTT CTTCTTTTCC TTCTTCTCTT CTTTCTGTCC TTTTCTCTCT CGTGCTTTAT 41460  
 TTCTTCTTCT TTCCCTGTGT TTCTTCTTCT TTTCTTTCTT CTCTGTTTCT TTTTCCCTTC 41520  
 TTTCTTCTCT TTCTTTCTCT ATTCTTCTCT TCTTTTTCTG TGTTTCTTTC CTTCCCGTCT 41580  
 GTCTTTTAAA AAATTGGAGT GTTTCAGAAG TTTACTTTGT GTATCTACGT TTTCTAAATT 41640  
 GTCTCTCTTT TCTCCATTTT CTCTCTCCCT CCCTCCCTCC CTCCCTGCTC CCTTCCCTCC 41700  
 CTCCTTCCCT TTCGCCATCT GTCTCTTTTC CCCACTCCCC TCCCCCGTC TGTCTCTGCG 41760  
 TGGATTCCGG AAGAGCCTAC CGATTCTGCC TCTCCGTGTG TCTGCAGCGA CCCCAGCACC 41820  
 GAGTCCTTGT GTGTTCTTTC TCCCTCCCTC CCTCCCTCCC TCCCTCCCTC CCTCCCTGCT 41880  
 TCCGAGAGGC ATCTCCAGAG ACCGCGCCGT GGGTTGTCTT CTGACTCTGT CGCGGTGAG 41940  
 GCAGAGACGC GTTTTGGGCA CCGTTTGTGT GGGGTTGGGG CAGAGGGGCT GCGTTTTCGG 42000  
 CCTCGGGAAG AGCTTCTCGA CTCACGGTTT CGTTTTCGCG GTCCACGGGC CGCCCTGCCA 42060  
 GCCGGATCTG TCTCGCTGAC GTCCGCGCGG GTTCTCGGGC TCCATCTGGC GCGCGCTTTG 42120  
 AGATCGTGCT CTCGGCTTCC GGAGCTGCGG TGGCAGCTGC CGAGGGAGGG GACCGTCCCC 42180  
 GCTGTGAGCT AGGCAGAGCT CCGGAAAGCC CGCGGTGCTC AGCCCGGCTG GCCCGGTGGC 42240  
 GCCAGAGCTG TGGCCGGTCT CTTGTGAGTC ACAGCTCTGG CGTGCAAGTT TATGTGGGGG 42300  
 AGAGGCTGTC GCTGCGCTTC TGGGCCCGCG GCGGCGCTGG GCGTCCCCGG GCCGTCGAC 42360  
 CAGCGCGCCG TAGCTCCCGA GGCCCGAGCC GCGACCCGGC GGACCCCGCG CGCGTGGCGG 42420

|            |            |            |            |            |            |       |
|------------|------------|------------|------------|------------|------------|-------|
| AGGCTGGGGA | CGCCCTTCCC | GGCCCGGTCG | CGGTCCGCTC | ATCCTGGCCG | TCTGAGGCGG | 42480 |
| CGGCCGAATT | CGTTTCCGAG | ATCCCCGTGG | GGAGCCGGGG | ACCGTCCCCG | CCCCGTCCCC | 42540 |
| CGGGTGCCCG | GGAGCGGTCC | CCGGGCCGGG | CCGCGGTCCC | TCTGCCCGCA | TCCTTTCTGG | 42600 |
| CGAGTCCCCG | TGGCCAGTCG | GAGAGCGCTC | CCTGAGCCGG | TGCGGCCCGA | GAGGTCGCGC | 42660 |
| TGGCCGGCCT | TCGGTCCCTC | GTGTGTCCCG | GTCGTAGGAG | GGGCCGGCCG | AAAATGCTTC | 42720 |
| CGGCTCCCGC | TCTGGAGACA | CGGGCCGGCC | CCTGCGTGTG | GCCAGGGCGG | CCGGGAGGGC | 42780 |
| TCCCCGGCCC | GGCGCTGTCC | CCGCGTGTGT | CCTTGGGTTG | ACCAGAGGGA | CCCCGGGCGC | 42840 |
| TCCGTGTGTG | GCTGCGATGG | TGGCGTTTTT | GGGGACAGGT | GTCCGTGTCC | GTGTCGCGCG | 42900 |
| TCGCCTGGGC | CGGCGGCGTG | GTCGGTGACG | CGACCTCCCC | GCCCCGGGGG | AGGTATATCT | 42960 |
| TTGCTCCGA  | GTCGGCAATT | TTGGGCCGCC | GGGTTATAT  |            |            | 42999 |

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTCCCCGCGG | GCCCCCGTGT | TCGCCGTTCC | CGTGGCGCGG | ACAATGCGGT | TGTGCGTCCA | 60  |
| CGTGTGCGTG | TCCGTGCAGT | GCCGTGTGTG | AGTGCCTCGC | TCTCCTCCTC | CTCCCCGGCA | 120 |
| GCGTTCCAC  | GGTTGGGGAC | CACCGGTGAC | CTCGCCCTCT | TCGGGCCTGG | ATCCG      | 175 |

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGTCTGGTGG | GAATTGTTGA | CCTCGCTCTC | GGGTGCGGCC | TTTGGGGAAC | GGCGGGGTCG | 60  |
| GTCGTGCCCC | GCGCCGGACG | TGTGTCGGGG | CCCACTTCCC | GCTCGAGGGT | GGCGGTGGCG | 120 |
| GCGGCGTTGG | TAGTCTCCCG | TGTTGCGTCT | TCCCGGGCTC | TTGGGGGGGG | TGCCGTCGTT | 180 |
| TTCGGGGCCG | GCGTTGCTTG | GCTTACGCAG | GCTTGTTTGG | GGACTGCCTC | AGGAGTCGTG | 240 |
| GGCGGTGTGA | TTCCCGCCCG | TTTTGCCCTC | CGTCTGCCTG | CTTTGCCTCG | GTTTGTCTTG | 300 |
| GTTCGTGTCT | CGGGAGCGGT | GGTTTTTTTT | TTTTTCGGGT | CCCGGGGAGA | GGGGTTTTTC | 360 |
| CGGGGGACGT | TCCCGTCGCC | CCCTGCCGCC | GGTGGGTTTT | CGTTTCGGGC | TGTGTTGCTT | 420 |
| TCCCCTTCCC | CGTTTCGCCG | TCGGTTCTCC | CCGGTCGGTC | GGCCCTCTCC | CCGGTCGGTC | 480 |
| GCCCGGCCGT | GCTGCCGGAC | CCCCCTTCT  | GGGGGGGATG | CCCGGGCACG | CACGCGTCCG | 540 |
| GGCGGCCACT | GTGGTCCGGG | AGCTGCTCGG | CAGGCGGGTG | AGCCAGTTGG | AGGGGCGTCA | 600 |
| TGCCCCCGCG | GGCTCCCGTG | GCCGACGCGG | CGTGTCTTTT | GGGGGGGCCT | GTGCGTGCGG | 660 |
| GAAGGCTGCG | CACGTTGTCT | GTCCTTGCGA | GGGAAAGAGG | CTTTTTTTTT | TTAGGGGGGT | 720 |
| GTCCTTCGTC | GTCCCGTCGG | CGGTGGATCC | GGCCT      |            |            | 755 |

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| GGCCGAGGTG | CGTCTGCGGG  | TTGGGGCTCG | TCCGGCCCCG | TCGTCTCCG   | GGAAGGCGTT | 60  |
| TAGCGGGTAC | CGTCGCCGCG  | CCGAGGTGGG | CGCACGTCGG | TGAGATAACC  | CCGAGCGTGT | 120 |
| TTCTGGTTGT | TGGCGGCGGG  | GGCTCCGGTC | GATGTCTTCC | CCTCCCCCTC  | TCCCCGAGGC | 180 |
| CAGGTCAGCC | TCCGCCTGTG  | GGCTTCGTCG | GCCGTCTCCC | CCCCCTCAC   | GTCCCTCGCG | 240 |
| AGCGAGCCCG | TCCGTTTCGAC | CTTCCTTCGG | CCTTCCCCCG | ATCTTTCCGC  | GCTCCGTTGG | 300 |
| CCCCGGGGTT | TTCACGGCGC  | CCCCACGCT  | CCTCCGCCTC | TCCGCCCCGTG | GTTTGGACGC | 360 |
| CTGGTTCCGG | TCTCCCCGCC  | AAACCCCGGT | TGGGTTGGTC | TCCGGCCCCG  | GCTTGCTCTT | 420 |
| CGGGTCTCCC | AACCCCCGGC  | CGGAAGGGTT | CGGGGGTTCC | GGG         |            | 463 |

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| GGATTCTTCA | GGATTGAAAC | CCAAACCGGT | TCAGTTTCTT  | TTCCGGCTCC | GGCCGGGGGG | 60  |
| GGCGGCCCCG | GGCGGTTTGG | TGAGTTAGAT | AACCTCGGGC  | CGATCGCACG | CCCCCGTG   | 120 |
| CGGCGACGAC | CCATTGGAAC | GTCTGCCCTA | TCAACTTTTCG | ATGGTAGTCG | ATGTGCCTAC | 180 |
| CATGGTGACC | ACGGGTGACG | GGAATCAGG  | GTTCGATTCC  | GGAGAGGGAG | CCTGAGAAAC | 240 |
| GGCTACCACA | TCCAAGGAAG | GCAGCAGGCG | CGCAAATTAC  | CCACTCCCGA | CCCGGGGAGG | 300 |
| TAGTGACGAA | AAATAACAAT | ACAGGACTCT | TTCGAGGCC   | TGTAATTGGA | ATGAGTCCAC | 360 |
| TTTAAATCCT | TTAAGCAG   |            |             |            |            | 378 |

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| GATCCATTGG | AGGGCAAGTC | TGGTGCCAGC | AGCCGCGGTA  | ATTCCAGCTC | CAATAGCGTA | 60  |
| TATTAAAGTT | GCTGCAGTTA | AAAAGCTCGT | AGTTGGATCT  | TGGGAGCGGG | CGGGCGGTCC | 120 |
| GCCGCGAGGC | GAGTCACCGC | CCGTCCCCGC | CCCTTGCCCTC | TCGGCGCCCC | CTCGATGCTC | 180 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TTAGCTGAGT | TGTCCCGCGG | GGCCCGAAGC | GTTTACTTTG | AAAAAATTAG | AGTTGTTTCA | 240 |
| AAGCAGGCC  | GAGCCGCTG  | GATACCGCCA | GCTAGGAAAT | AATGGAATAG | GACCGCGGTT | 300 |
| CCTATTTTGT | TTGGTTTTCG | GAAGTGAAGC | CATGATTAAG | GGAAACGGCC | GGGGGCATTG | 360 |
| CCTTATTGCG | CCCCCCTA   |            |            |            |            | 378 |

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGATCTTTCC | CGCTCCCCGT | TCCTCCCGGC | CCCTCCACCC | GCGCGTCTCC | CCCCTTCTTT | 60  |
| TCCCCTCTCC | GGAGGGGGGG | GAGGTGGGGG | CGCGTGGGCG | GGGTCGGGGG | TGGGGTCGGC | 120 |
| GGGGGACCGC | CCCCGGCCCG | CAAAAGGCCG | CCGCCGGGCG | CACTTCAACC | GTAGCGGTGC | 180 |
| GCCGCGACCG | GCTACGAGAC | GGCTGGGAAG | GCCCGACGGG | GAATGTGGCT | CGGGGGGGGC | 240 |
| GGCGCGTCTC | AGGGCGCGCC | GAACCACCTC | ACCCGAGTGT | TTACAGCCCT | CCGGCCCGCG | 300 |
| TTTCGCGGAA | TCCCGGGGCC | GAGGGGAAGC | CCGATACCCG | TCGCCGCGCT | TTTCCCCTCC | 360 |
| CCCCGTCCGC | CTCCCGGGCG | GGCGTGGGGG | TGGGGGCCGG | GCCGCCCTC  | CCACGCCCGT | 420 |
| GGTTTCTCTC | TCTCCCGGTC | TCGGCCGGTT | TGGGGGGGGG | AGCCCGGTTG | GGGGCGGGGC | 480 |
| GGACTGTCTT | CAGTGCGCC  | CGGCGTCTGT | CGCGCCGTCG | GGCCCGGGGG | GTTCTCTCGG | 540 |
| TCACGCCGCC | CCCGACGAAG | CCGAGCGCAC | GGGGTCGGCG | GCGATGTCGG | CTACCCACCC | 600 |
| GACCCGTCTT | GAAACACGGA | CCAAGGAGTC | TAACGCGTGC | GCGAGTCAGG | GGCTCGCACG | 660 |
| AAAGCCGCCG | TGGCGCAATG | AAGGTGAAGG | GCCCCGTCCG | GGGGCCCGAG | GTGGGATCC  | 719 |

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CGAGGCCTCT | CCAGTCCGCC | GAGGGCGCAC | CACCGGCCCG | TCTCGCCCGC | CGCGTCGGGG | 60  |
| AGGTGGAGCA | CGAGCGTACG | CGTTAGGACC | CGAAAGATGG | TGAAGTATGC | CTGGGCAGGG | 120 |
| CGAAGCCAGA | GGAAACTCTG | GTGGAGGTCC | GTAGCGGTCC | TGACGTGCAA | ATCGGTCGTC | 180 |
| CGACCTGGGT | ATAGGGGCGA | AAGACTAATC | GAACCATCTA | GTAGCTGGTT | CCCTCCGAAG | 240 |
| TTTCCCTCAG | GATAGCTGGC | GCTCTCGCAA | CCTTCGGAAG | CAGTTTATC  | CGGGTAAAGG | 300 |
| CGGAATGGAT | TAGGAGGTCT | TGGGGCCGGA | AACGATCTCA | AACTATTTCT | CAAACCTTAA | 360 |
| ATGGGTAAGG | AAGCCCGGCT | CGCTGGCGTG | GAGCCGGGCG | TGGAATGCGA | GTGCCTAGTG | 420 |
| GGCCACTTTT | GGTAAGCAGA | ACTGGCGCTG | CGGGATGAAC | CGAACGCCCG | GTTAAGGCGC | 480 |
| CCGATGCCGA | CGCTCATCAG | ACCCAGAAA  | AGGTGTTGGT | TGATATAGAC | AGCAGGACGG | 540 |
| TGGCCATGGA | AGTCGGAATC | CGCTAAGGAG | TGTGTAACAA | CTCACCTGCC | GAATCAACTA | 600 |
| GCCCTGAAAA | TGGATGGCGC | TGGAGCGTCG | GGCCCATACC | CGGCCGTCGC | CGGCAGTCGG | 660 |
| AACGGGACGG | GACGGGAGCG | GCCGC      |            |            |            | 685 |

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG

33

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG

35

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC

33

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC

34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCTT AACCTTAACC CTAACCCTAA  
CCCTAACCTT AACCCGGGAT

60

80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGGCCCTA GGCTTAAGG

19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

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